



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:19 PM UTC

PDB ID : 7AJU / pdb_00007aju
EMDB ID : EMD-11808
Title : Cryo-EM structure of the 90S-exosome super-complex (state Post-A1-exosome)
Authors : Cheng, J.; Lau, B.; Flemming, D.; Venuta, G.L.; Berninghausen, O.; Beckmann, R.; Hurt, E.
Deposited on : 2020-09-29
Resolution : 3.80 Å (reported)
Based on initial model : 6ZQD

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

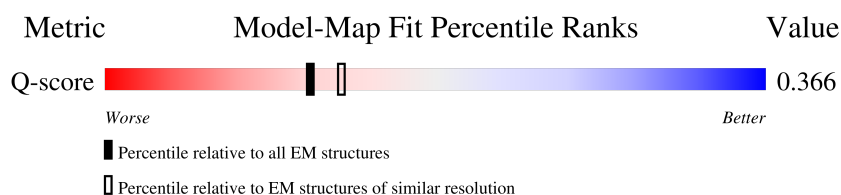
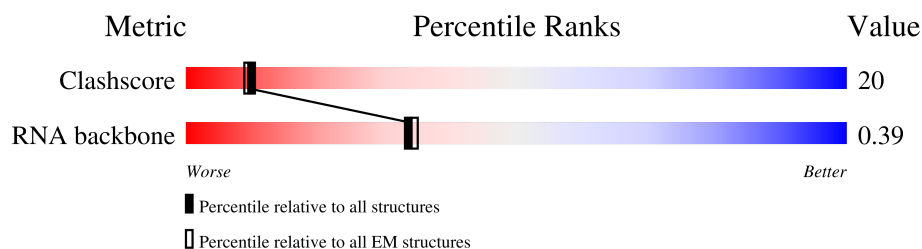
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

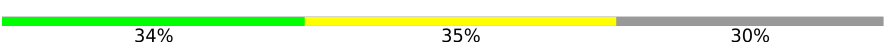
The reported resolution of this entry is 3.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



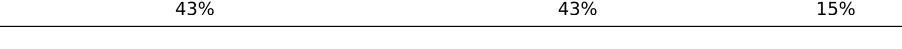
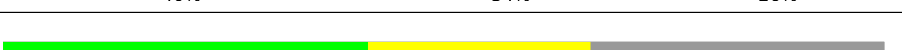
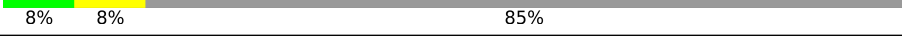
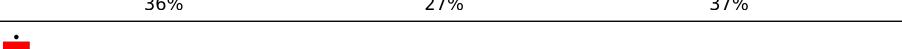
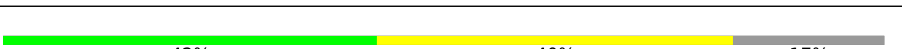
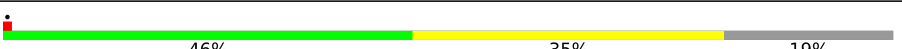
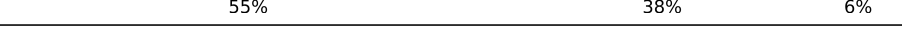
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
RNA backbone	8273	3508	-
Q-score	-	25397	10198 (3.30 - 4.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	CA	327	
1	CB	327	
2	DA	255	
3	UA	923	

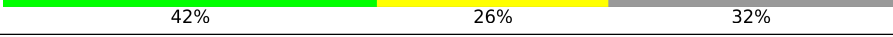
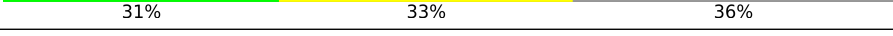
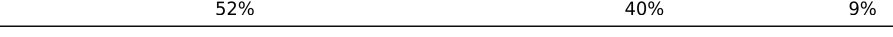
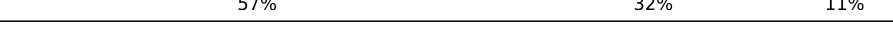
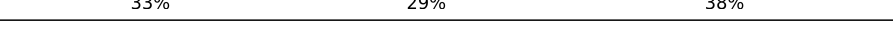
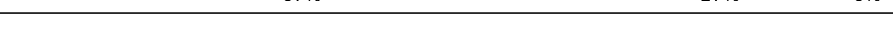
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	UB	810	
5	UC	610	
6	UD	776	
7	UE	643	
8	UF	440	
9	UG	554	
10	UH	713	
11	UI	575	
12	UJ	1769	
13	UK	250	
14	UL	943	
15	UM	817	
16	UN	899	
17	UO	513	
18	UP	214	
19	UQ	896	
20	UR	594	
21	US	552	
22	UT	2493	
23	UU	939	
24	UV	1237	
25	UX	189	
26	CD	504	
27	CE	511	
28	CF	126	

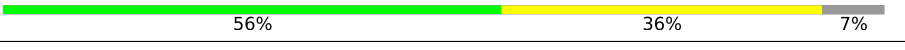
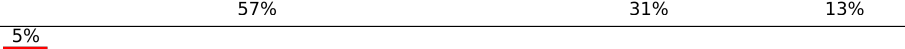
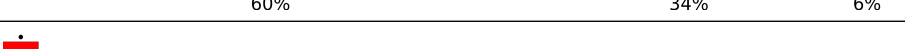
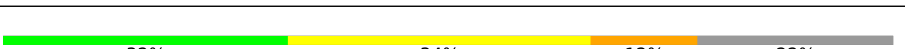
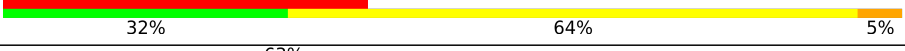
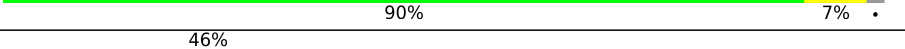
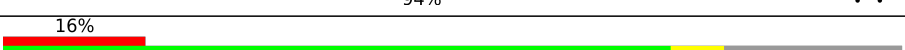
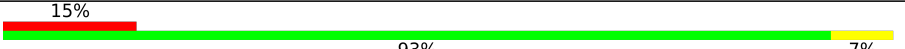
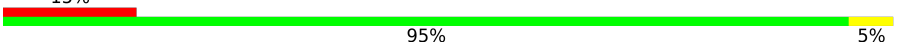
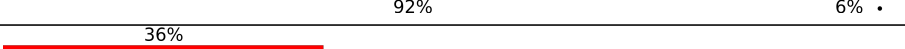
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
28	CG	126	
29	CH	573	
30	CI	183	
31	CJ	290	
32	CK	593	
33	CL	1183	
34	CM	367	
35	CN	297	
36	JD	1267	
37	JF	252	
37	JG	252	
38	JH	483	
39	JI	1729	
40	JL	318	
41	JM	217	
42	JP	489	
43	Db	82	
44	JJ	274	
45	DE	261	
46	DF	225	
47	DG	236	
48	DH	190	
49	DI	200	
50	DJ	197	
51	DL	156	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
52	DN	151	
53	DO	137	
54	DQ	143	
55	DS	146	
56	DT	144	
57	DW	130	
58	DX	145	
59	DY	135	
60	Dc	67	
61	D2	81	
62	D3	1802	
63	D4	333	
64	EA	22	
65	EB	305	
66	EC	246	
67	ED	394	
68	EE	223	
69	EF	265	
70	EG	250	
71	EH	240	
72	EI	359	
73	EJ	292	
74	EK	1001	
75	EN	1073	

2 Entry composition [i](#)

There are 78 unique types of molecules in this entry. The entry contains 242031 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CA	242	Total	C	N	O	S	0	0
			1881	1193	338	340	10		
1	CB	228	Total	C	N	O	S	0	0
			1782	1131	320	321	10		

- Molecule 2 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	DA	240	Total	C	N	O	S	0	0
			1912	1209	354	345	4		

- Molecule 3 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	UA	792	Total	C	N	O	S	0	0
			6322	4040	1083	1181	18		

- Molecule 4 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	UB	553	Total	C	N	O	S	0	0
			4105	2602	736	756	11		

- Molecule 5 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	UC	86	Total	C	N	O	0	0
			694	430	139	125		

- Molecule 6 is a protein called U3 small nucleolar RNA-associated protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	UD	663	Total	C	N	O	S	0	0
			5269	3339	915	994	21		

- Molecule 7 is a protein called U3 small nucleolar RNA-associated protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	UE	475	Total	C	N	O	S	0	0
			3772	2400	649	710	13		

- Molecule 8 is a protein called U3 small nucleolar RNA-associated protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	UF	293	Total	C	N	O	S	0	0
			2487	1605	435	434	13		

- Molecule 9 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	UG	470	Total	C	N	O	S	0	0
			3718	2345	664	698	11		

- Molecule 10 is a protein called U3 small nucleolar RNA-associated protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	UH	474	Total	C	N	O	S	0	0
			2771	1706	513	549	3		

- Molecule 11 is a protein called U3 small nucleolar RNA-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	UI	88	Total	C	N	O	S	0	0
			723	462	131	128	2		

- Molecule 12 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	UJ	1116	Total	C	N	O	S	0	0
			8961	5802	1468	1666	25		

- Molecule 13 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	UK	219	Total	C	N	O	S	0	0
			1845	1150	356	332	7		

- Molecule 14 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	UL	779	Total	C	N	O	S	0	0
			6199	3974	1034	1164	27		

- Molecule 15 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	UM	762	Total	C	N	O	S	0	0
			5970	3787	1007	1148	28		

- Molecule 16 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	UN	203	Total	C	N	O	S	0	0
			1667	1038	313	314	2		

- Molecule 17 is a protein called U3 small nucleolar RNA-associated protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	UO	493	Total	C	N	O	S	0	0
			3911	2462	702	735	12		

- Molecule 18 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	UP	60	Total	C	N	O	0	0
			495	310	101	84		

- Molecule 19 is a protein called NET1-associated nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	UQ	820	Total	C	N	O	S	0	0
			6557	4171	1107	1260	19		

- Molecule 20 is a protein called U3 small nucleolar RNA-associated protein 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	UR	481	Total	C	N	O	S	0	0
			3791	2399	668	714	10		

- Molecule 21 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	US	487	Total	C	N	O	S	0	0
			3587	2305	610	660	12		

- Molecule 22 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	UT	2313	Total	C	N	O	S	0	0
			18789	12100	3144	3479	66		

- Molecule 23 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	UU	878	Total	C	N	O	S	0	0
			6922	4386	1198	1316	22		

- Molecule 24 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	UV	1083	Total	C	N	O	S	0	0
			8753	5692	1442	1595	24		

- Molecule 25 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	UX	167	Total	C	N	O	S	0	0
			1330	854	241	225	10		

- Molecule 26 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	CD	380	Total	C	N	O	S	0	0
			2994	1898	513	574	9		

- Molecule 27 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	CE	436	Total	C	N	O	S	0	0
			3326	2093	571	654	8		

- Molecule 28 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	CF	121	Total	C	N	O	S	0	0
			916	583	158	171	4		
28	CG	121	Total	C	N	O	S	0	0
			916	583	158	171	4		

- Molecule 29 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	CH	467	Total	C	N	O	S	0	0
			3736	2371	655	700	10		

- Molecule 30 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	CI	175	Total	C	N	O	S	0	0
			1468	929	276	256	7		

- Molecule 31 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	CJ	256	Total	C	N	O	S	0	0
			2081	1306	394	374	7		

- Molecule 32 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	CK	222	Total	C	N	O	S	0	0
			1789	1111	311	363	4		

- Molecule 33 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	CL	808	Total	C	N	O	S	0	0
			6551	4187	1171	1165	28		

- Molecule 34 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	CM	360	Total	C	N	O	S	0	0
			2781	1781	473	516	11		

- Molecule 35 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	CN	229	Total	C	N	O	S	0	0
			1868	1197	317	347	7		

- Molecule 36 is a protein called Probable ATP-dependent RNA helicase DHR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	JD	811	Total	C	N	O	S	0	0
			6509	4163	1151	1160	35		

- Molecule 37 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	JF	216	Total	C	N	O	S	0	0
			1701	1079	296	315	11		
37	JG	230	Total	C	N	O	S	0	0
			1799	1142	313	333	11		

- Molecule 38 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	JH	261	Total	C	N	O	0	0
			1295	773	261	261		

- Molecule 39 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	JI	265	Total	C	N	O	0	0
			1314	784	265	265		

- Molecule 40 is a protein called Dimethyladenosine transferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	JL	283	Total	C	N	O	S	0	0
			2262	1439	401	408	14		

- Molecule 41 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	JM	134	Total	C	N	O	S	0	0
			1131	715	206	207	3		

- Molecule 42 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	JP	461	Total	C	N	O	S	0	0
			3765	2354	686	709	16		

- Molecule 43 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Db	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 44 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	JJ	199	Total	C	N	O	S	0	0
			1573	1001	285	283	4		

- Molecule 45 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	DE	246	Total	C	N	O	S	0	0
			1950	1248	361	338	3		

- Molecule 46 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	DF	213	Total	C	N	O	S	0	0
			1669	1045	307	314	3		

- Molecule 47 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	DG	218	Total	C	N	O	S	0	0
			1755	1102	337	313	3		

- Molecule 48 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	DH	170	Total	C	N	O	0	0
			1361	880	235	246		

- Molecule 49 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	DI	177	Total	C	N	O	S	0	0
			1399	869	279	249	2		

- Molecule 50 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	DJ	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 51 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	DL	140	Total	C	N	O	S	0	0
			1129	724	215	187	3		

- Molecule 52 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	DN	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 53 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	DO	127	Total	C	N	O	S	0	0
			922	567	185	167	3		

- Molecule 54 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	DQ	125	Total	C	N	O	0	0
			969	623	174	172		

- Molecule 55 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	DS	105	Total	C	N	O	S	0	0
			861	545	160	154	2		

- Molecule 56 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	DT	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 57 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	DW	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 58 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	DX	143	Total	C	N	O	S	0	0
			1115	705	219	189	2		

- Molecule 59 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
59	DY	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 60 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Dc	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 61 is a RNA chain called 5'ETS RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	D2	81	Total	C	N	O	P	0	0
			1741	777	319	564	81		

- Molecule 62 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	D3	1409	Total	C	N	O	P	0	0
			30042	13429	5342	9862	1409		

- Molecule 63 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	D4	223	Total	C	N	O	P	0	0
			4720	2113	816	1568	223		

- Molecule 64 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	EA	22	Total	C	N	O	P	0	0
			366	161	43	140	22		

- Molecule 65 is a protein called Exosome complex component RRP45.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	EB	299	Total	C	N	O	P	0	0
			1475	877	299	299			

- Molecule 66 is a protein called Exosome complex component SKI6.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	EC	243	Total	C	N	O	P	0	0
			1199	713	243	243			

- Molecule 67 is a protein called Exosome complex component RRP43.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	ED	317	Total	C	N	O	P	1	0
			1571	937	317	317			

- Molecule 68 is a protein called Exosome complex component RRP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	EE	223	Total	C	N	O	P	1	0
			1107	661	223	223			

- Molecule 69 is a protein called Exosome complex component RRP42.

Mol	Chain	Residues	Atoms				AltConf	Trace
69	EF	265	Total	C	N	O	1	0
			1317	787	265	265		

- Molecule 70 is a protein called Exosome complex component MTR3.

Mol	Chain	Residues	Atoms				AltConf	Trace
70	EG	215	Total	C	N	O	0	0
			1058	628	215	215		

- Molecule 71 is a protein called Exosome complex component RRP40.

Mol	Chain	Residues	Atoms				AltConf	Trace
71	EH	237	Total	C	N	O	0	0
			1170	696	237	237		

- Molecule 72 is a protein called Exosome complex component RRP4.

Mol	Chain	Residues	Atoms				AltConf	Trace
72	EI	293	Total	C	N	O	0	0
			1440	854	293	293		

- Molecule 73 is a protein called Exosome complex component CSL4.

Mol	Chain	Residues	Atoms				AltConf	Trace
73	EJ	222	Total	C	N	O	0	0
			1091	647	222	222		

- Molecule 74 is a protein called Exosome complex exonuclease DIS3.

Mol	Chain	Residues	Atoms				AltConf	Trace
74	EK	970	Total	C	N	O	1	0
			4818	2878	970	970		

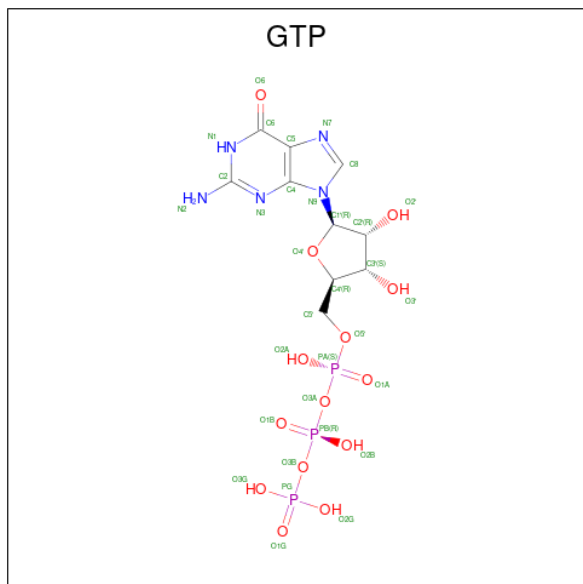
- Molecule 75 is a protein called ATP-dependent RNA helicase DOB1.

Mol	Chain	Residues	Atoms				AltConf	Trace
75	EN	963	Total	C	N	O	0	0
			4762	2839	963	960		

- Molecule 76 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
76	UX	1	Total	Zn	0
			1	1	
76	Db	1	Total	Zn	0
			1	1	
76	EK	1	Total	Zn	0
			1	1	

- Molecule 77 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
77	CL	1	Total	C	N	O	P	0
			32	10	5	14	3	

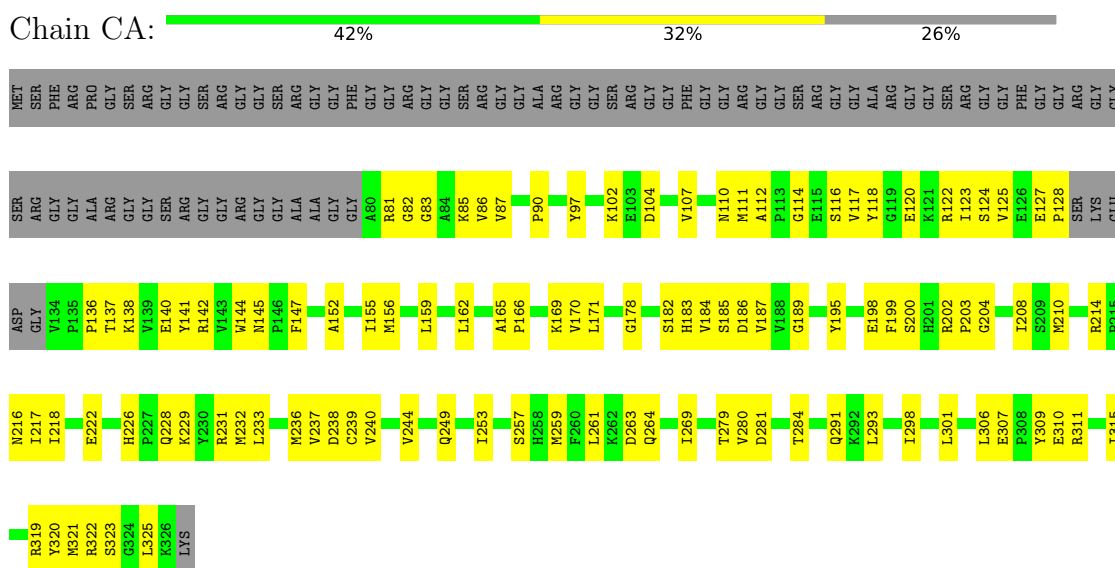
- Molecule 78 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
78	CL	1	Total	Mg	0
			1	1	
78	EK	1	Total	Mg	0
			1	1	

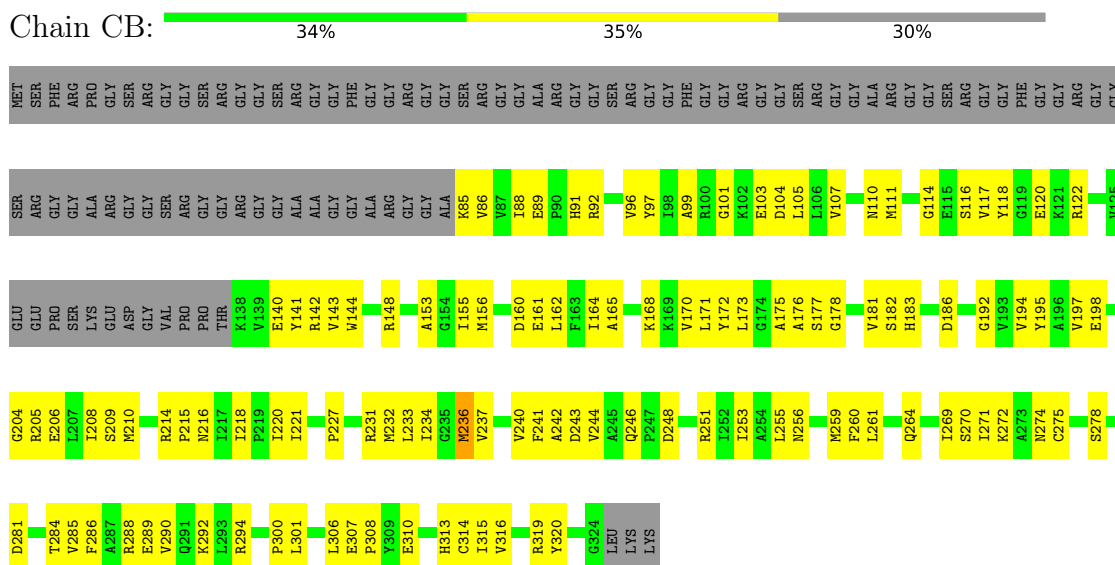
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

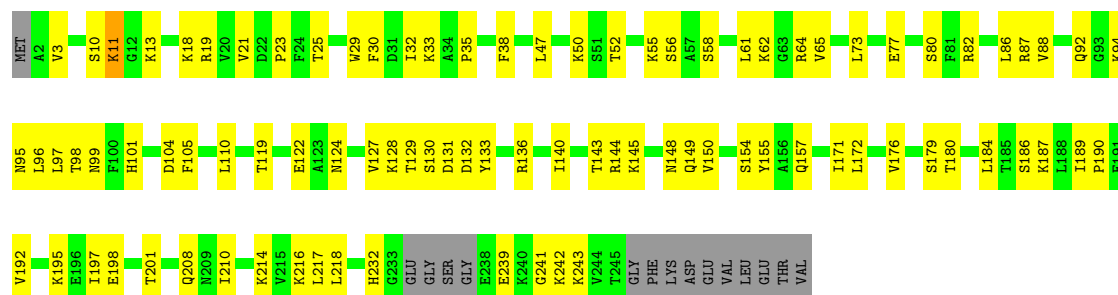
• Molecule 1: rRNA 2'-O-methyltransferase fibrillarin



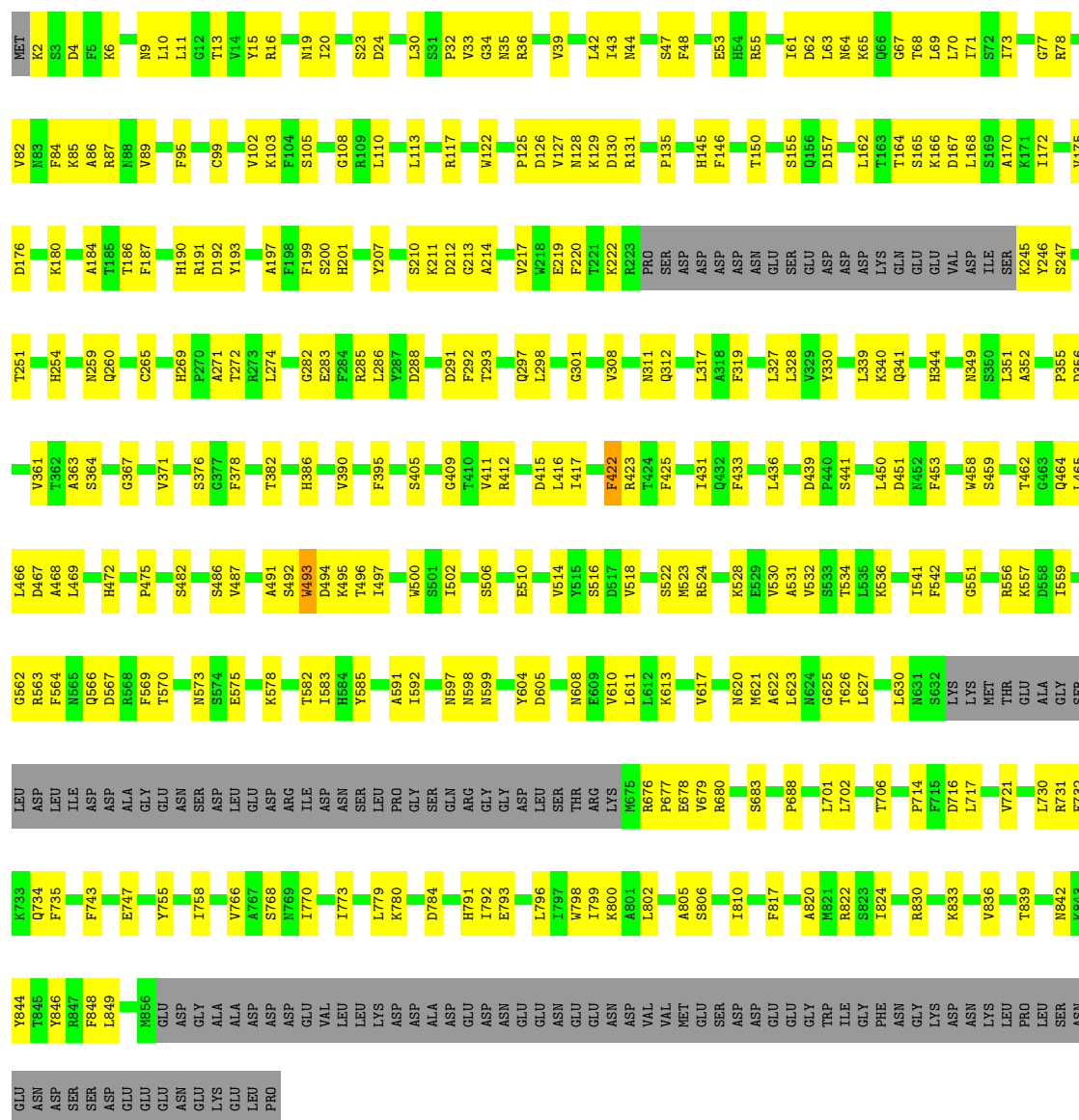
• Molecule 1: rRNA 2'-O-methyltransferase fibrillarin



Chain DA:

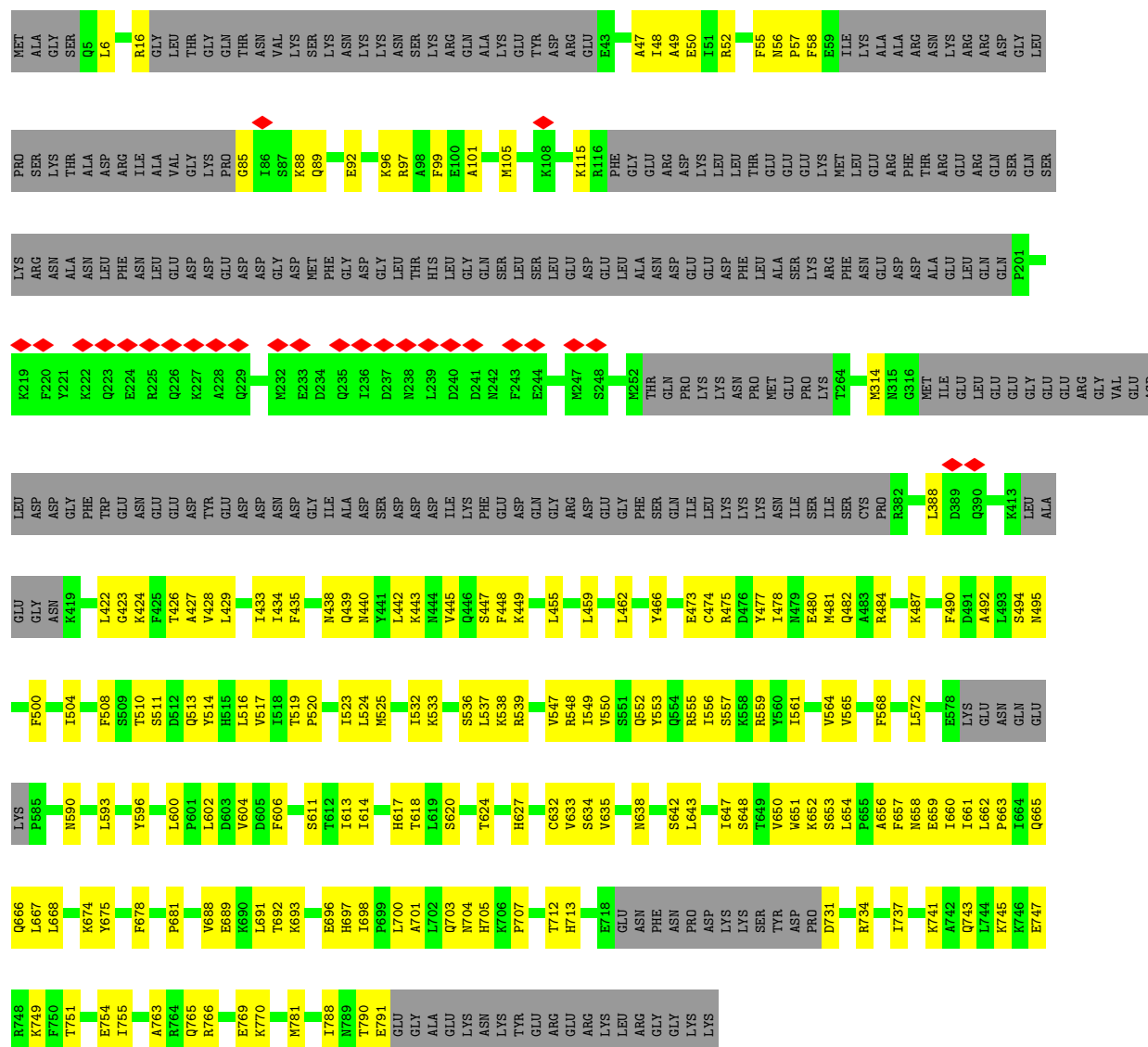


Chain UA:



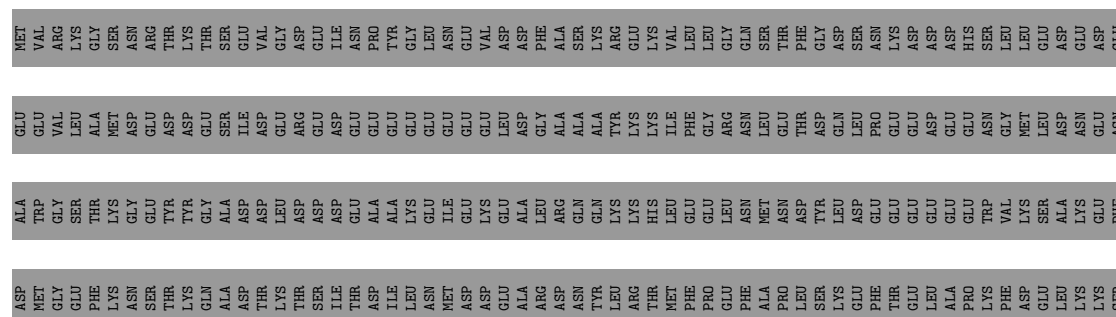
• Molecule 4: Nucleolar complex protein 14

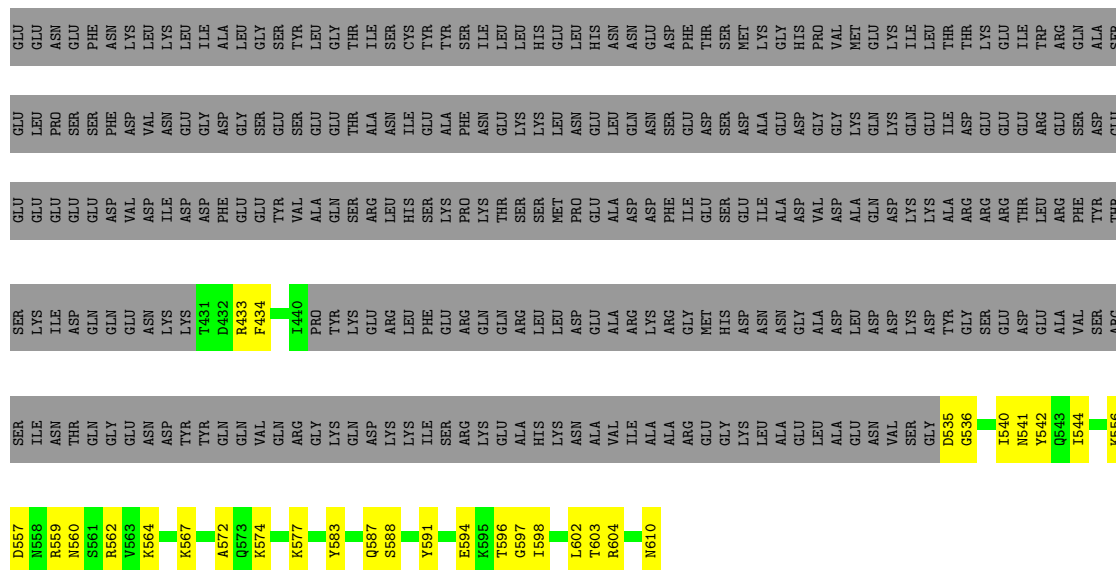
Chain UB:



• Molecule 5: Something about silencing protein 10

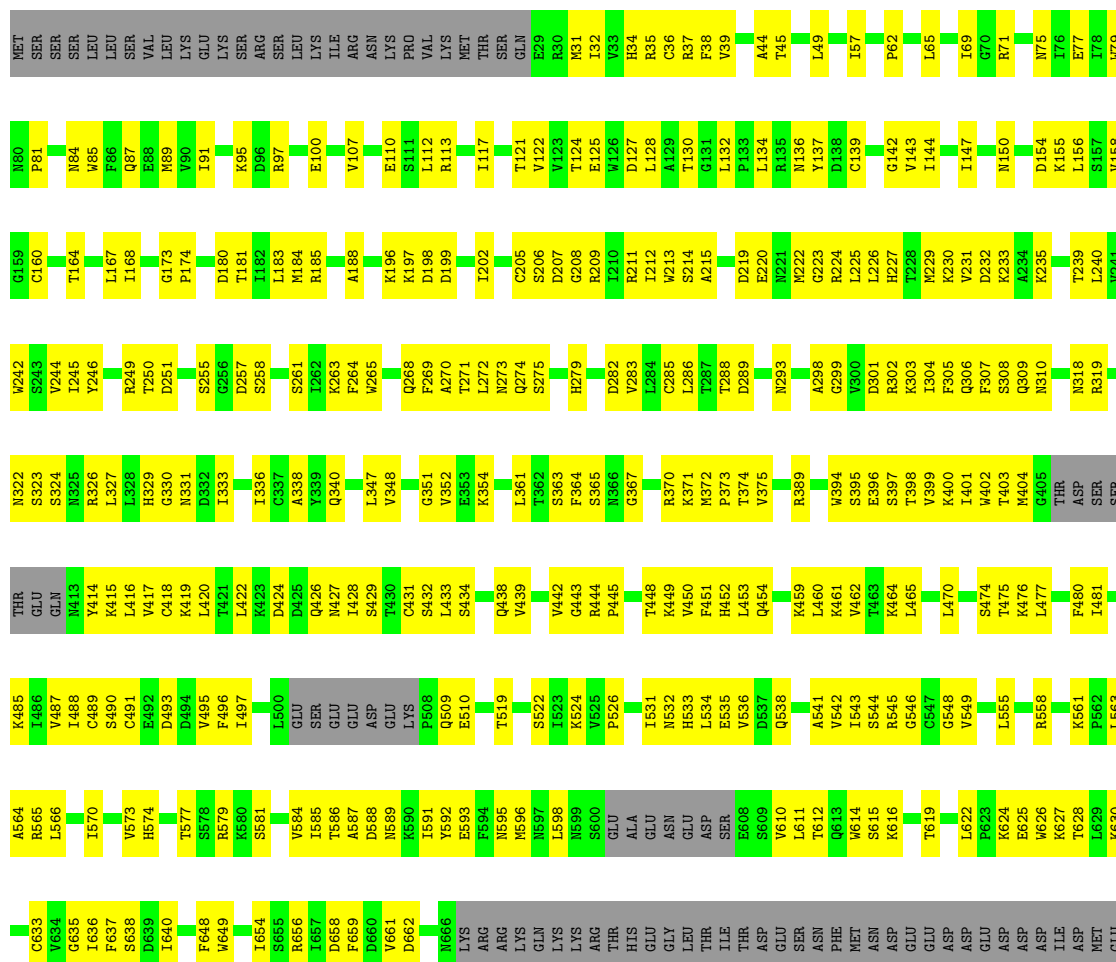
Chain UC:

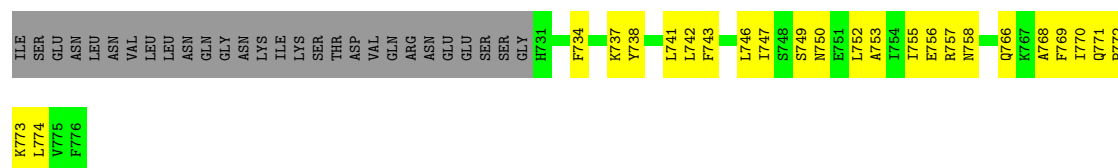




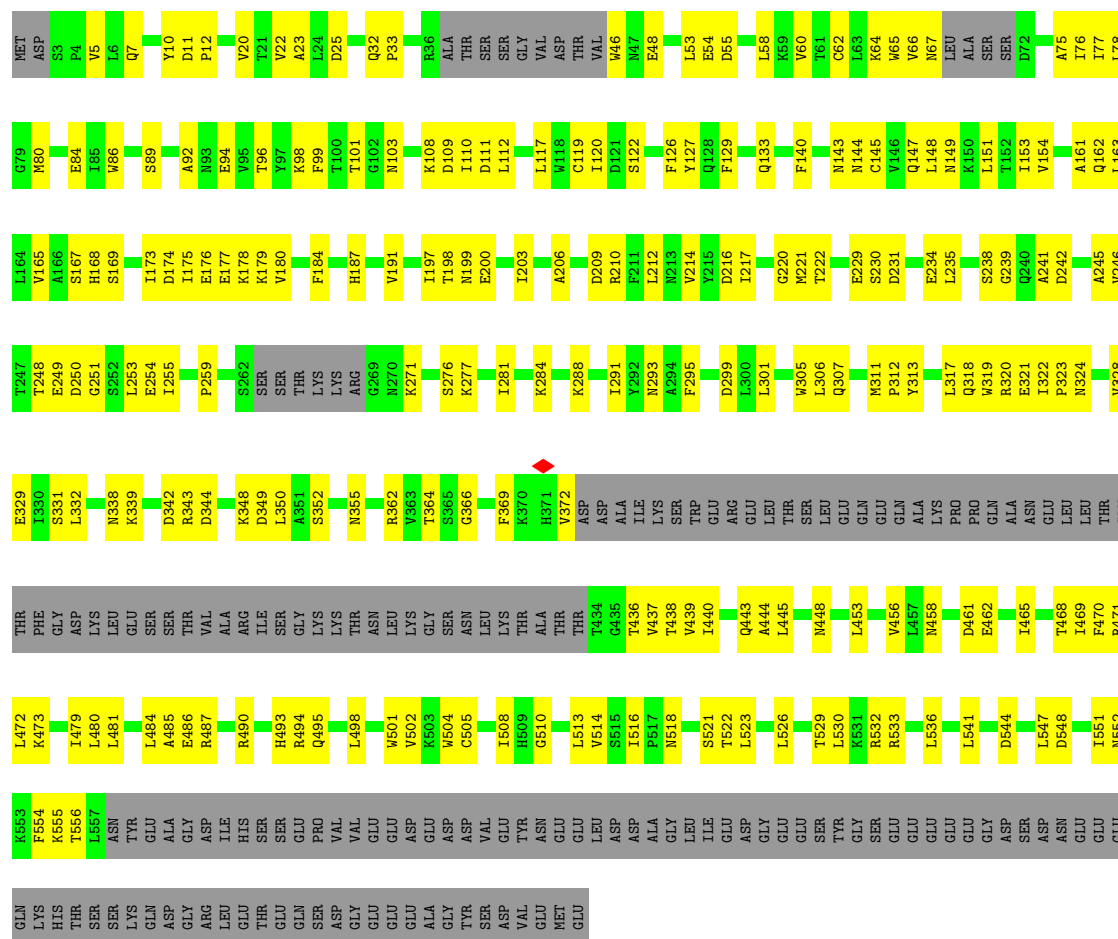
• Molecule 6: U3 small nucleolar RNA-associated protein 4

Chain UD: 43% 43% 15%

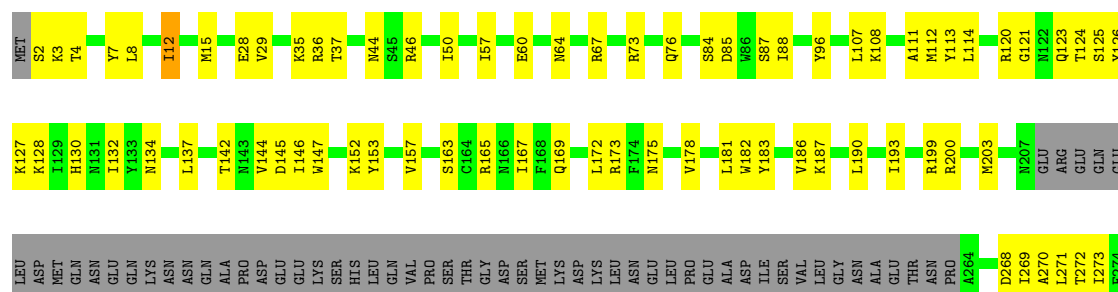


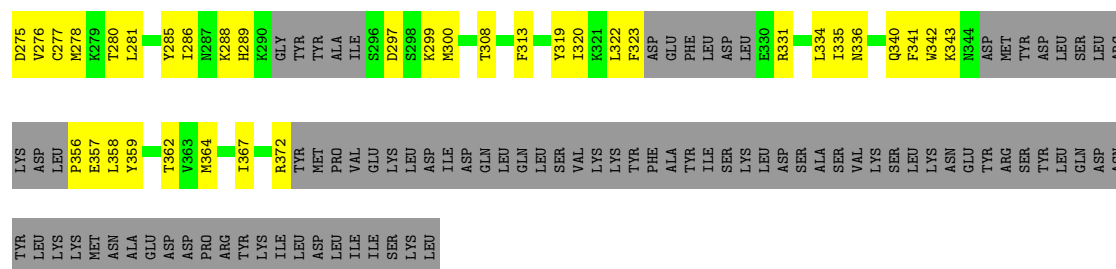


• Molecule 7: U3 small nucleolar RNA-associated protein 5



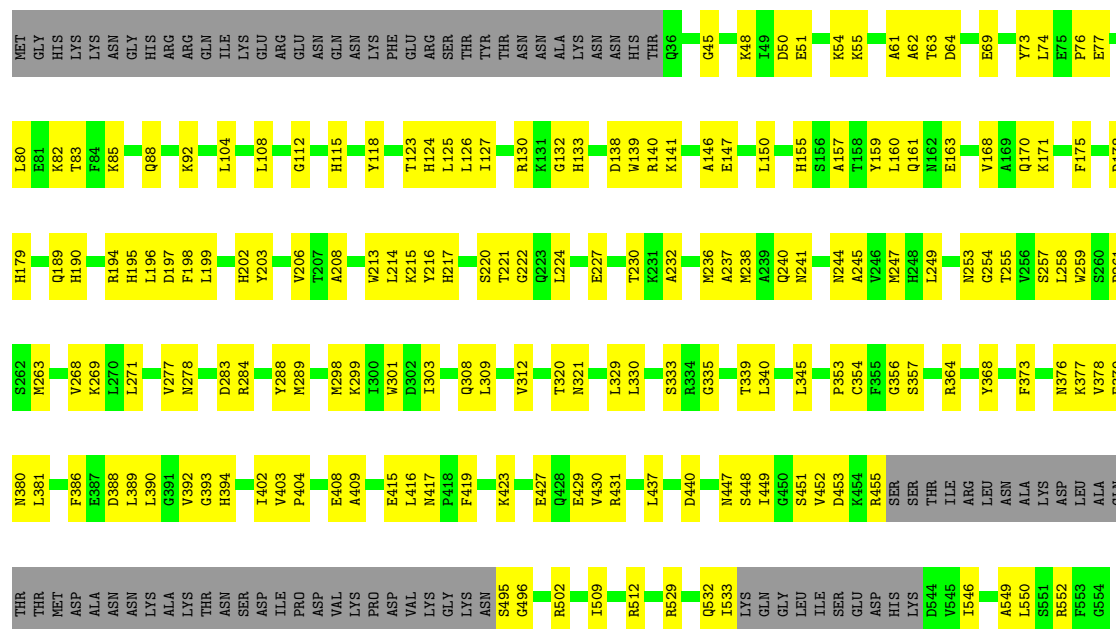
• Molecule 8: U3 small nucleolar RNA-associated protein 6





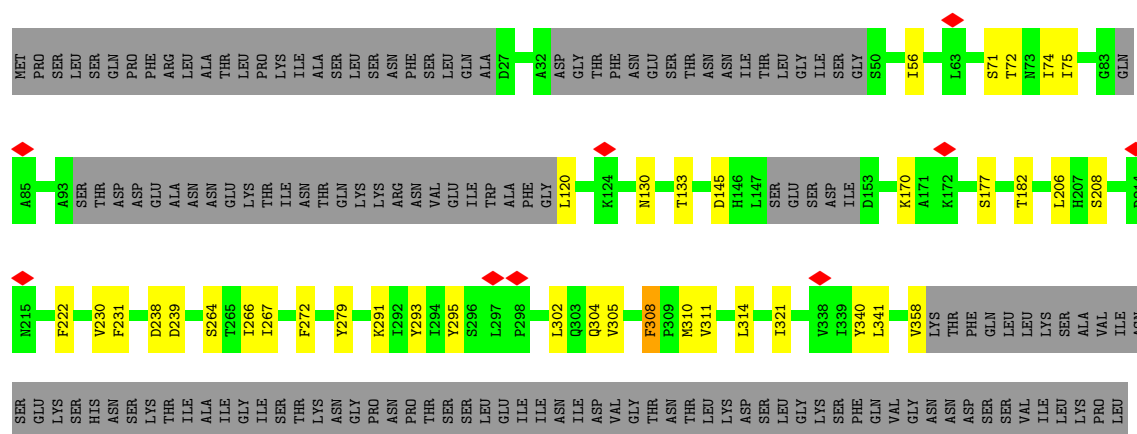
• Molecule 9: U3 small nucleolar RNA-associated protein 7

Chain UG:

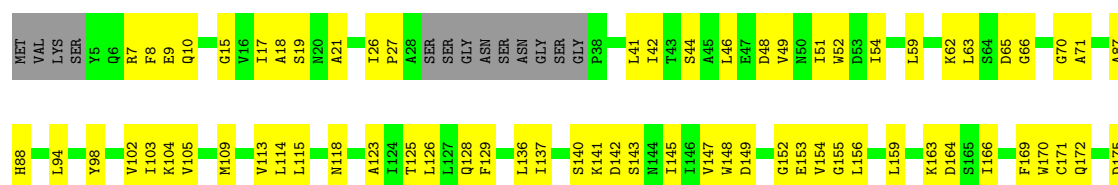


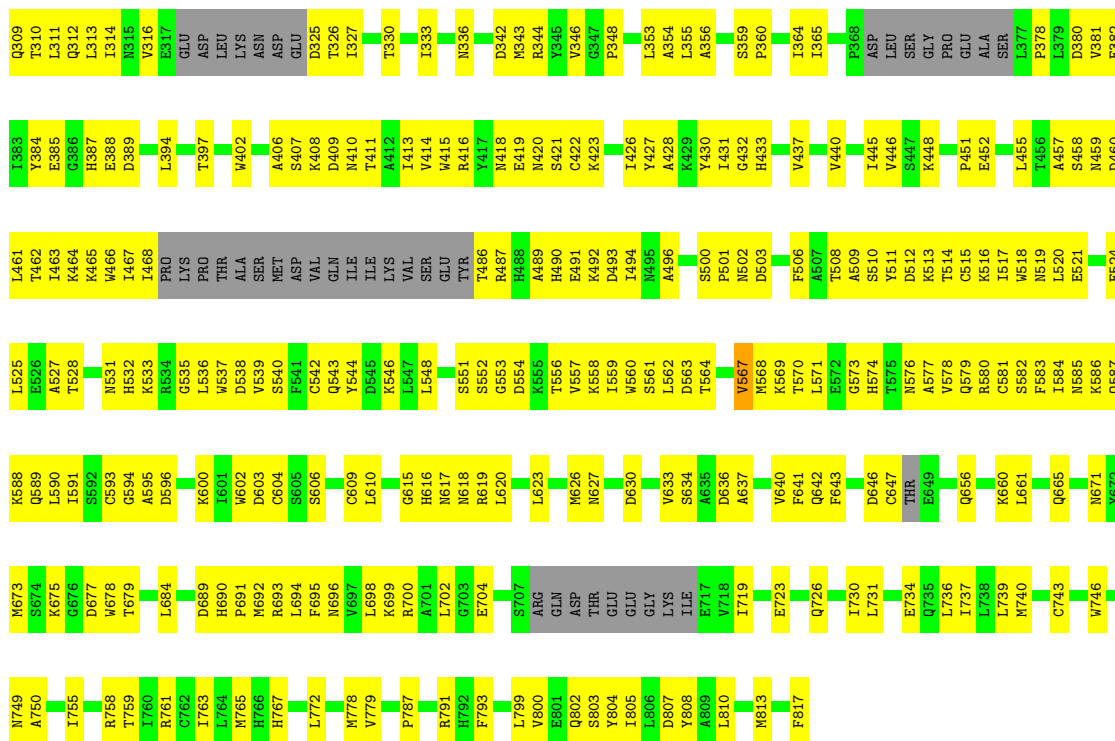
• Molecule 10: U3 small nucleolar RNA-associated protein 8

Chain UH:

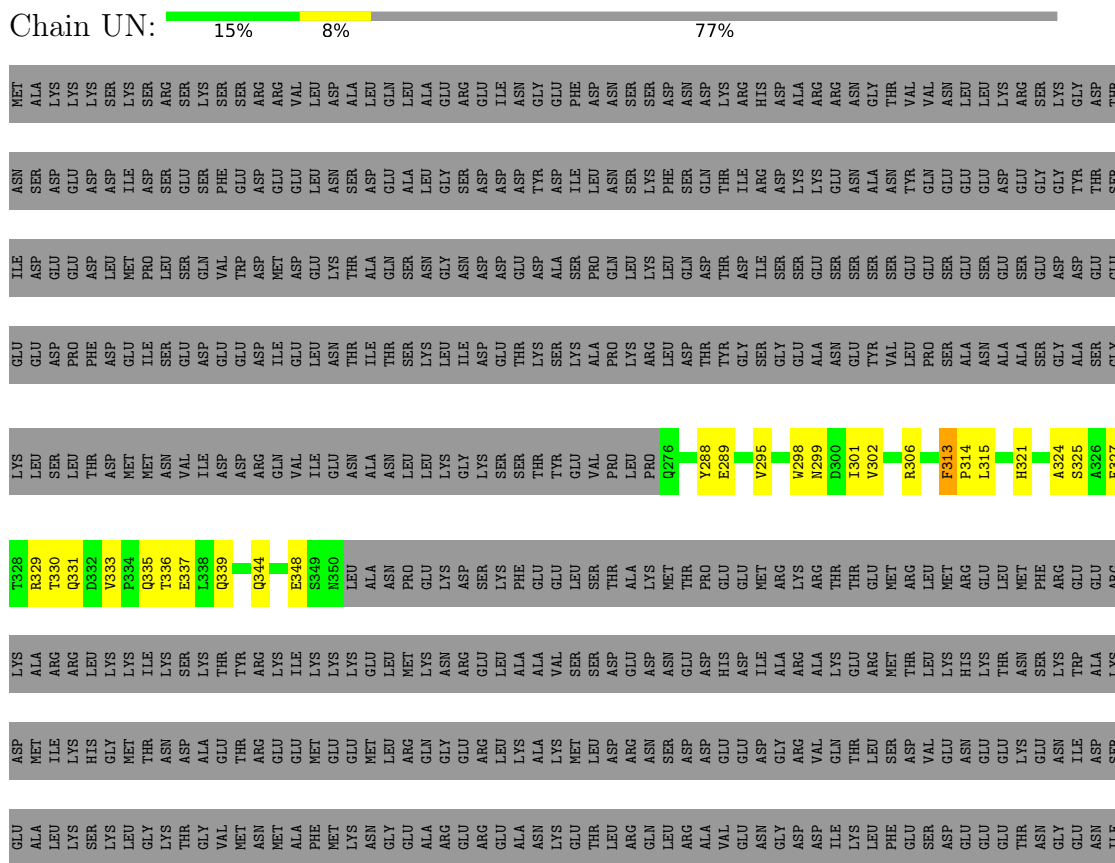








- Molecule 16: U3 small nucleolar RNA-associated protein 14





SER	ASP
GLU	GLN
VAL	LYS
GLU	ASP
SER	GLY
GLU	GLY
GLY	GLY
GLY	GLY
THR	SER
THR	THR
GLN	GLN
ARG	GLN
GLU	TYR
GLU	TYR
GLU	SER
ALA	SER
ALA	SER
ILE	ARG
ARG	ARG
LEU	VAL
LEU	VAL
ARG	ASP
SER	GLY
LYS	SER
ARG	ASP
ARG	GLY
LYS	ASN
GLN	GLU
GLU	GLU
ASN	ALA
GLU	ALA
LEU	ALA
TYR	LYS
LYS	LYS
LYS	LYS
SER	VAL
VAL	ASN
GLU	GLY
THR	THR
GLY	GLY
VAL	VAL
THR	THR
ASP	ASP
GLU	VAL
VAL	ILE
ALA	ALA
GLU	GLU
LEU	LEU
PRO	PRO
GLU	GLY
GLY	GLY
LEU	LEU
LEU	LEU
LYS	LYS
ASN	ASN
ILE	ILE

T189	T190	P191	P192	K193	K194	E195	S196	S197	T198	T199	K200	W205	R208	K209	A210	L211	R212	K213	G214
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

● Molecule 19: NET1-associated nuclear protein 1

Chain UQ: 48% 43% 8%

NET	THR	GLN	SER	LEU	GLY	ILE	GLU	Q9	K11	G17	G18	K19	P20	A21	L22	S26	S27	V28	K32	R36	L37	S38	Q41	R42	R43	I46	P47	F48	M49	V64	Y65	S56	V57	E58	T59	R60	Q61	C62	V63	K64	F68	M71	S72	L73	L74	S75	Q80
-----	-----	-----	-----	-----	-----	-----	-----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

E83	T88	W89	K90	I91	L92	L93	T97	Y98	Q101	GLU	ASP	A104	T108	T111	R112	N113	G114	H115	V116	T117	V118	P129	K130	H131	F132	K133	D138	E139	D214	K140	Y151	R152	L153	L154	T155	T156	F157	K158	D159	PRO	SER	GLN	LYS	ALA	HIS	N166	S167	L168	Q169	S170	Y171	R172
-----	-----	-----	-----	-----	-----	-----	-----	-----	------	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------

L173	Y174	A175	L176	T177	F178	D179	K183	Q184	F185	E186	L187	A188	H189	Q190	A191	E192	W193	H194	N195	V196	T197	L198	S199	N200	N204	L207	L208	W211	C212	D214	V215	S216	T217	K218	D219	H220	E221	H222	K223	S224	V228	S229	L230	F231	L237	S238	L244	T249
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

L252	S253	Y254	N255	K256	R257	Y259	M262	L263	D264	D265	M266	M267	G268	Q269	Q270	L271	F275	L357	L358	Q359	N360	T361	E362	N363	N366	S367	D368	Y369	Q370	F371	L372	S299	V300	L301	S302	L303	S304	F305	S306	H307	S310	Y311	L312	L313	S314	W317	K397	H398	K319	V320	K321	S322	L323	W324
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

Q325	L326	S330	Q331	Q332	F333	L334	P335	R336	L337	G338	T340	I341	I342	D343	V346	L356	L357	L358	Q359	N360	T361	E362	N363	N366	S367	D368	Y369	Q370	F371	L372	S375	L379	K382	L383	S384	L385	N386	G387	P388	V391	T395	I396	K397	H398	L399	Q400	Q401	S404
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

A405	M406	M407	T408	K409	M410	S411	M412	S413	T414	T415	S416	L417	Q424	S425	R426	K427	L428	T429	K430	S431	R432	R433	Q434	D435	F436	T437	V440	E441	T442	M443	P444	K447	Y450	H453	T459	F460	D461	K464	M465	M469	Y470	Q471	Y472	L473	M478	M479	S480	V484	R485
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

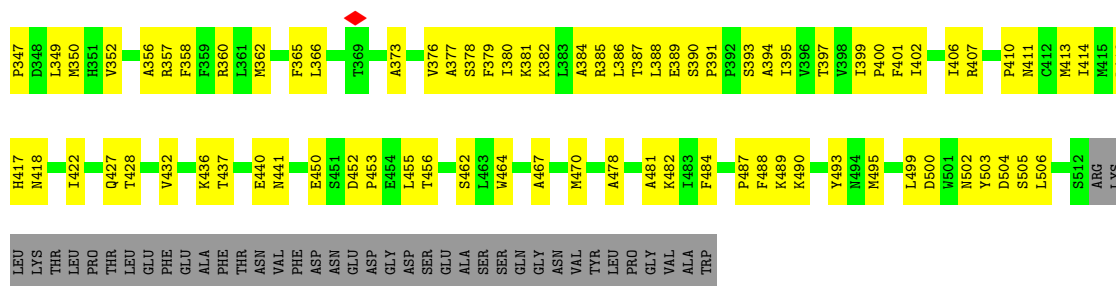
L488	I495	T496	D497	L498	K499	F500	K502	W506	M507	L508	D509	Y510	E511	L519	S520	S521	S522	H527	E528	L529	K530	F531	W532	T533	K534	N535	E538	W541	T545	K546	V547	P550	H551	S554	L557	T558	K559	L560	L561	P562	S563	P564	R565	S566	V567	Q571
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

L574	T575	A576	N577	N578	N579	G580	G581	L582	K583	F584	W585	S586	F587	D588	Y589	H590	E591	S592	N593	W594	K597	K598	S600	L601	P602	V603	F604	N605	H606	S612	L613	A614	W615	H624	D627	D628	K629	L630	Q631	I632	T637	F638	K639	K640	F641	E642	E645	N646	T647	K648
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

S651	E652	F653	T654	D655	D656	S657	E658	L659	Q660	L664	L665	N669	L670	E761	Y762	T763	W764	W765	I766	G767	W768	N769	L770	D771	W772	D773	F774	L775	F776	L777	D778	L694	Y695	V698	N699	K703	H706	M707	D714	E715	L716	T717	G718	W719	I720	I724	D730	LEU	ASP	GLY	W734
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	------

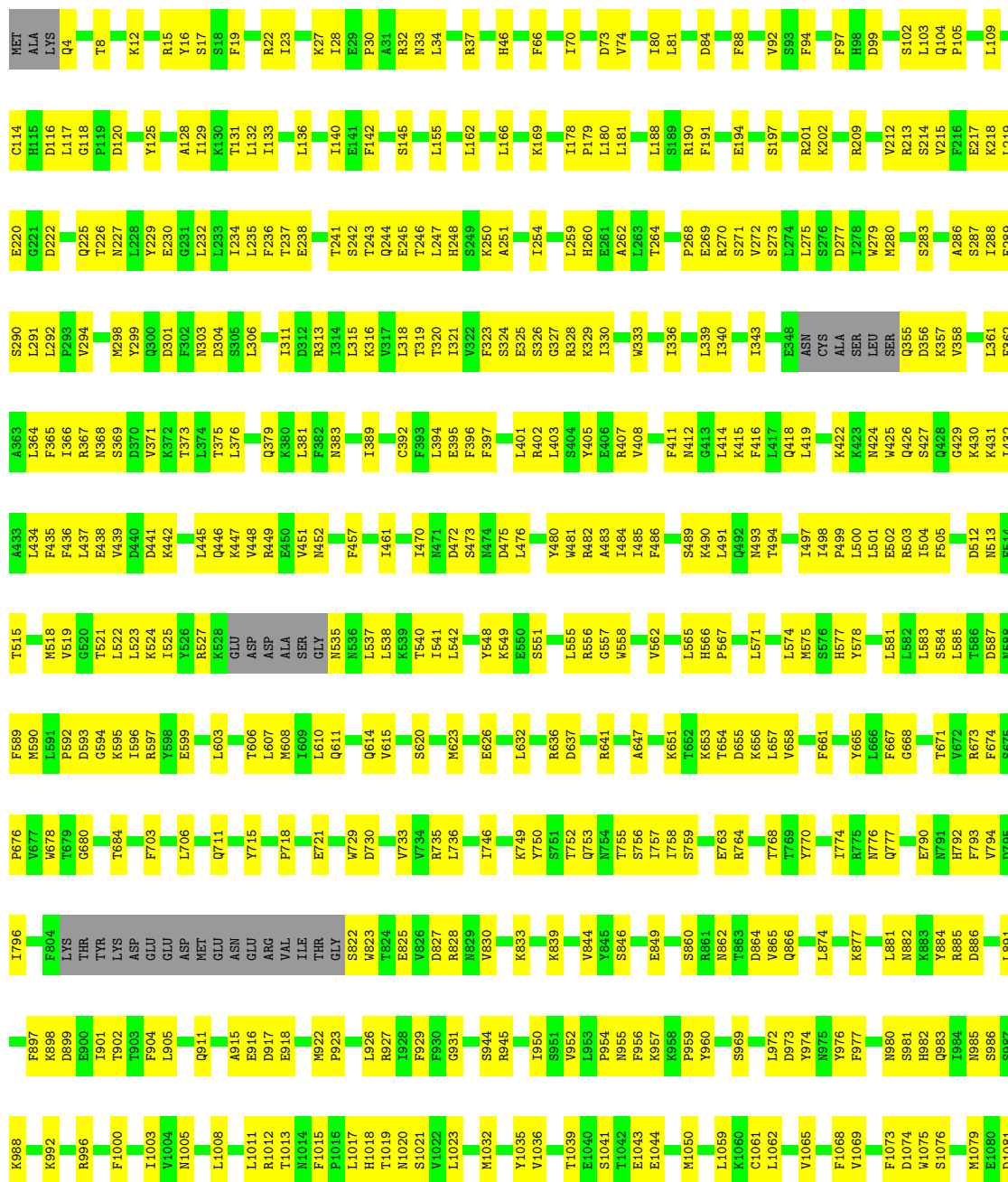
I737	K740	S741	R742	T745	F746	D747	S748	D749	L754	H760	E761	Y762	T763	W764	W765	I766	G767	W768	N769	L770	D771	W772	D773	F774	L775	F776	L777	D778	L694	Y695	V698	N699	K703	H706	M707	D714	E715	L716	T717	G718	W719	I720	I724	D730	LEU	ASP	GLY	W734
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	------

VAL	SER	ASN	THR	ILE	THR	THR	THR	THR	ALA	ALA	ASN	SER	ASP	ASP	ILE	PHE	ALA	GLY	GLN	LEU	HIS	LYS	LYS	SER	ARG	GLY	LYS	LYS	ASP	THR	THR	ASP	ASP	LYS	ASN	THR	ASN	ASN	ASP	N646	E851	E852	I853	F857	K863	D864	N868	S871	F872	M875	F876	D877	I879
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------



• Molecule 22: U3 small nucleolar RNA-associated protein 20

Chain UT: 50% 42% 7%



G2234	K2166	E2081	P1988	L1887	R1780	L1670	Y1591	Q1508	A1367	L1304	G1236	H1166	I1082
I2235	V2167	L2085	D1989	L1888	I1781	V1671	P1592	I1509	S1368	V1305	E1237	Y1167	Y1083
T2237	Y2168	I2086	L1990	T1889	M782	K1675	T1593	Q1516	H1369	A1306	N1238	V1168	A1084
C2238	K2170	I2087	Q1996	S1890	L1783	K1675	S1594	Q1517	A1370	D1307	D1239	D1169	V1085
L2240	S2171	T2088	G1997	H1891	E1791	R1683	S1596	M1518	T1371	M1309	L1240	L1170	V1087
Y2241	I1E	K2089	L1998	L1792	L1793	G1684	K1596	H1517	M1372	S1310	Q1241	V1171	K1088
PR0	GLY	A2090	A1999	L1794	R1794	Q1686	I1597	Y1523	K1373	Y1311	K1242	L1172	P1089
H2243	E2175	L2095	F2000	R1795	R1601	S1685	R1601	Y1529	T1375	S1312	I1244	L1174	I1090
L2263	H2176	S2096	N2001	L1899	D1602	Q1686	D1602	R1529	F1377	S1314	K1245	G1175	I1091
V2264	T2177	K2097	F2002	L1903	E1604	V1689	E1604	S1532	A1378	R1315	L1246	T1176	S1095
H2285	E2179	S2098	L2003	L1904	T1605	T1693	T1605	M1533	ASP	M1316	L1247	S1177	D1096
Q2256	L2180	S2099	L2006	S1905	I1606	L1698	I1607	T1536	PHE	H1317	I1250	E1097	N1098
K2261	D2181	A2105	K2009	E1906	E1608	K1699	K1537	K1537	THR	D1320	V1251	K1180	I1181
ASP	E2182	L2106	H2010	N1907	M1610	M1701	M1610	K1542	VAL	F1321	W1258	L1185	Q1101
LYS	L2183	V2109	T2011	Y1910	M1611	H1702	P1611	V1545	ASN	R1323	I1261	Y1186	S1103
GLY	A2184	S2110	L2019	T1914	L1621	L1710	L1621	P1554	ILE	L1324	E1262	L1189	L1106
THR	T2185	F2111	A2020	L1915	G1622	S1714	G1622	P1555	Q1458	L1325	E1263	S1190	H1114
GLU	K2186	N2112	D2021	R1916	T1623	M1716	T1623	L1556	G1463	L1326	L1264	D1191	P1102
ILE	T2187	D2113	T2022	I1917	N1625	I1717	N1625	E1587	Q1463	T1327	Y1265	S1192	P1102
SER	L2188	L1918	L2023	L1918	L1628	M1722	L1628	L1559	Q1463	F1328	T1266	S1193	P1116
LEU	R2189	L1919	R2024	L1919	F1631	M1723	F1631	V1562	R1468	K1329	T1267	S1194	P1116
THR	Y2190	S1925	ASN	T1920	L1632	N1724	L1632	R1563	L1469	G1330	I1268	S1194	S1117
N2270	T2195	L2125	SER	L1921	L1635	A1729	L1635	ASP	G1478	TYR	E1277	I1195	L1118
GLY	VAL	L2130	GLY	L1924	L1636	K1741	L1636	GLY	N1479	SER	E1278	S1196	L1119
GLY	GLY	P2131	H2031	L1925	L1637	V1742	L1637	ALA	S1480	E1341	N1279	F1197	Q1120
SER	SER	K2132	S2032	F1926	T1637	K1743	T1637	GLU	E1481	L1342	R1281	T1129	F1121
L2133	GLU	L2133	K2033	S1927	L1638	E1744	Q1641	LYS	S1482	E1343	V1282	G1209	A1132
HIS	HIS	E2034	E2034	D1928	L1639	I1745	V1642	LEU	H1483	E1344	L1283	F1210	L1133
Q2202	Q2202	N2135	T2035	E1929	L1640	K1746	L1640	LEU	Y1484	L1345	L1284	I1211	M1134
Q2203	Q2203	K2136	R2036	S1930	L1641	S1747	S1645	SER	L1485	L1347	E1286	D1214	D1135
D2204	D2204	D2137	R2040	K1935	L1642	N1748	K1646	LYS	I1489	L1348	L1287	H1215	T1136
L2205	L2205	L2138	M2048	R1935	L1643	K1749	S1647	PHE	F1494	F1349	F1288	V1216	
S2208	S2208	E2139	E2049	R1939	L1644	N1750	R1651	ASP	S1495	T1350	I1289	R1217	V1142
T2212	T2212	I2140	Y2050	K1940	L1645	I1761	D1652	ASN	ASP	F1351	E1290	S1218	K1143
F2213	F2213	E2142	D2051	V1941	L1646	S1762	R1655	LEU	ASP	L1352	L1291	I1221	I1147
S2214	S2214	A2146	Q2052	L1942	L1647	L1763	R1655	ASP	E1498	I1355	G1292	S1222	G1148
S2215	S2215	L2149	R2056	N1943	L1648	L1764	R1655	ASP	E1498	M1356	K1294	I1225	I1151
Y2216	Y2216	L2149	K2059	I1944	L1649	L1765	S1662	PR0	R1499	M1357	V1295	S1226	A1152
M2217	M2217	L2149	Q2060	P1949	L1650	F1766	S1662	SER	TYR	K1358	P1296	E1227	A1153
T2220	T2220	GLN	Q2060	K1961	L1651	F1766	S1662	PR0	R1501	E1359	L1298	L1228	L1228
SER	SER	ASP	F2061	K1961	L1652	L1769	R1655	PR0	N1502	E1360	E1299	A1155	A1155
VAL	VAL	N2154	V2065	S1964	L1653	L1769	R1655	PR0	N1502	L1361	S1300	L1232	S1156
TYR	TYR	A2155	D2066	F1966	L1654	L1776	G1665	PR0	N1502	L1361	S1300	L1232	S1156
L2158	L2158	L2158	L2068	F1966	L1655	L1776	G1665	PR0	N1502	L1361	S1300	L1232	S1156
L2159	L2159	L2159	Q2069	F1966	L1656	L1776	G1665	PR0	N1502	L1361	S1300	L1232	S1156
L2160	L2160	L2160	Y2070	T1970	L1657	L1776	G1665	PR0	N1502	L1361	S1300	L1232	S1156
PRO	PRO	G2161	P2071	T1970	L1658	L1776	G1665	PR0	N1502	L1361	S1300	L1232	S1156
L2162	L2162	L2162	R2076	L1983	L1659	L1776	G1665	PR0	N1502	L1361	S1300	L1232	S1156
R2163	R2163	L2163	R2076	L1983	L1660	L1776	G1665	PR0	N1502	L1361	S1300	L1232	S1156
T2164	T2164	L2164	R2076	L1983	L1661	L1776	G1665	PR0	N1502	L1361	S1300	L1232	S1156
ASP	ASP	Y2165	M2080	L1987	L1662	L1776	G1665	PR0	N1502	L1361	S1300	L1232	S1156
D2233	D2233	Y2165	M2080	L1987	L1663	L1776	G1665	PR0	N1502	L1361	S1300	L1232	S1156



Chain UV:

45%

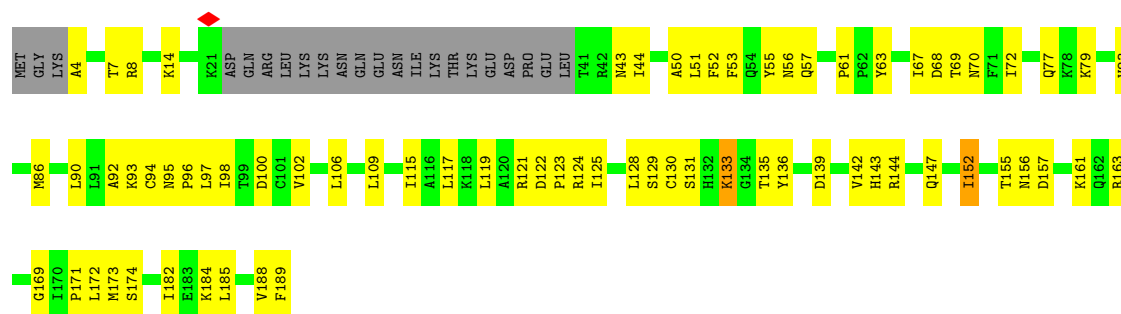
42%

12%

MET	ALA	THR	SER	VAL	LYS	ARG	LYS	ALA	SER	GLU	THR	ASP	GLN	ASN	ILE	VAL	LYS	VAL	GLN	LYS	HIS	THR	GLN	ASP	ILE	THR	GLN	ASP	GLU	ASN	HIS	SER	SER	GLN	ALA	ILE	GLU	ARG	THR	VAL	PRO	GLU	GLN	GLU	ASN	ASP	GLU	SER	THR										
K123	V124	K125	K126	F127	L128	H129	K130	L131	D132	D133	L134	L135	Q136	E137	I138	P139	D140	W141	K144	S145	L146	A147	E148	S151	F152	F153	K154	N155	K156	I157	S158	V159	V160	P161	F162	P167	I168	F169	T172	N173	F176	Y177	K178	P179	K180	P181	D182	I183	Q184	L185	I186	F189	A190						
L191	K192	A193	G194	Q197	P198	M199	G200	S201	S202	I203	D204	L205	L206	L207	T208	M209	P210	L213	F214	E215	K216	K217	D218	F219	R223	K224	L225	H226	K227	R228	S229	V230	Y231	L232	A233	T236	H237	H238	I241	L242	L243	K244	D245	D246	K247	L248	L252	Q253	S254	L255	E256	F259							
D260	L268	R269	I270	S271	C272	S273	K274	PRO	THR	GLY	ASP	SER	LEU	SER	D282	Y283	N284	F285	Y286	K287	T288	R289	F290	S291	L292	L294	L295	L296	Q297	F298	P299	Y300	K301	ASN	V302	F303	S304	P305	K306	K307	L308	L309	P310	N311	N312	N313	R316	I317	ALA	GLN	GLU	GLN	GLU	LYS	GLU	GLN	SER	GLN	L326
P327	A328	L331	L337	S338	S339	S340	H341	T342	H342	E343	Y344	Y345	L346	K347	L348	L349	K350	K351	T352	V360	V364	R367	L368	W369	L370	Q371	Q372	Q373	S376	N377	N378	M379	H381	S382	G383	S384	L385	G386	G387	F388	T389	F391	E392	F393	T394	I395	L396	M397	A398	A399	L400	L401							
N402	I406	K410	I411	L412	L413	H414	G415	F416	S417	Q420	L421	F422	K423	G424	V425	I426	K427	Y428	L429	D433	L434	H439	L440	Q441	S444	M445	PRO	L525	GLU	ASN	SER	SER	SER	P453	Y457	I458	D459	E460	T466	L467	F468	D469	K470	S471	T472	K473	V474	N475	L476	L477	L478	T479							
K479	Y485	E490	Y491	A492	G493	T495	L496	A497	M498	L499	M500	N501	D505	I510	P511	N514	I515	S516	R517	F518	D519	N520	L521	K522	Y523	D524	C526	Y527	D528	V529	Q530	L531	P532	L533	G534	K535	Y536	N537	N538	L539	L543	A544	A545	C546	M550	E551	R552	V553	I556	T557									
L558	E559	F561	L562	I566	V569	L574	P575	R576	D576	R577	I578	K579	F580	I581	G582	I583	E584	V585	Q587	Q588	D591	F592	F593	I594	R597	A598	V599	G605	F608	F609	D611	F612	V613	R614	V615	K616	L617	L618	V619	S622	E623	C624	D625	K626	L627	A633	H634	S635											
E636	F637	M638	A643	K646	H647	F648	R656	R657	F658	K659	T664	H665	C666	W669	S670	T671	I677	L681	V682	Q683	N683	L686	H689	K692	Q695	I696	S697	N698	K703	F704	P709	L710	N711	N712	T719	S720	V721	L722	N723	L730	F734	R735	S826	R827	D828														
I741	M744	S749	I753	L754	P755	S758	R761	Y762	T763	S764	L765	P768	D777	F778	F779	Q780	D781	V782	E787	K791	W792	D794	E795	S798	L799	K801	A805	F806	L807	L808	K809	B813	L814	N817	Y821	F825	S826	R827	D828																				
E829	S830	I831	E836	I837	H838	T839	L842	L843	T844	G847	R853	E854	T856	E857	R858	D859	L862	R865	A866	I867	A870	R871	N872	E873	L874	K875	L878	L883	A884	F885	Y889	R894	L899	E900	N901	I902	S903	H904	S905	Y906	Q907	V912	V913	R914	L915	F916													
K917	R918	D921	H923	L924	L925	L926	G927	H928	T929	E932	L933	A934	E935	L936	T937	A938	I939	K940	F942	V943	E944	P945	F949	L950	P951	L954	E955	N956	K960	Y961	L962	P965	W970	K971	P974	L975	L976	L977	D978	R981	P982	E983	ASP	ILE	ARG	ASP	THR												
PHE	GLU	THR	ILE	ALA	GLY	GLY	SER	GLU	LEU	ASP	SER	LYS	MET	THR	LYS	LEU	SER	I1010	R1011	L1012	T1013	Q1016	Y1017	K1018	G1019	M1022	N1023	F1024	I1025	N1026	ASN	L1027	S1030	D1031	P1032	N1033	L1037	Q1038	V1041	K1044	N1045	G1049	I1050	L1051	I1056	L1057	R1063	L1067											
V1070	L1080	N1081	Q1082	T1084	I1085	N1086	L1087	D1097	F1098	V1099	D1100	D1101	L1102	R1103	T1104	P1105	K1109	G1113	I1114	L1115	S1116	ALA	THR	GLU	PHE	LYS	ASN	ILE	THR	ASN	ASP	GLN	A1128	N1135	L1136	N1137	S1140	E1141	D1144	P1145	T1146	K1151	Y1152	L1153	N1154	L1155	K1156	Y1157	K1158	N1159									

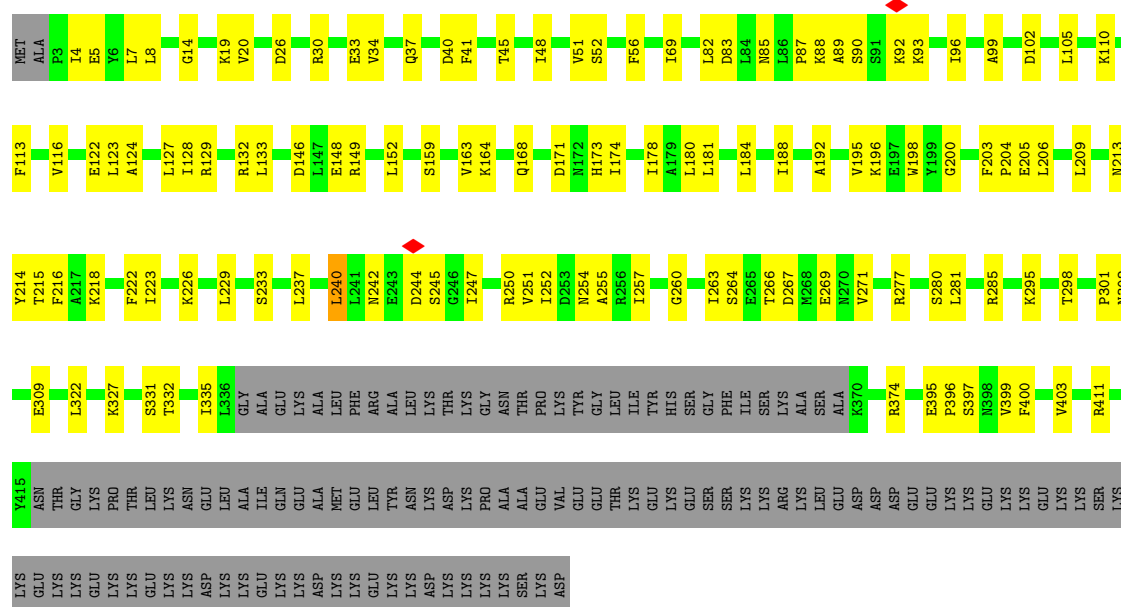
- Molecule 25: rRNA-processing protein FCF1

Chain UX:

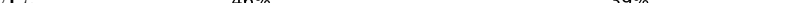


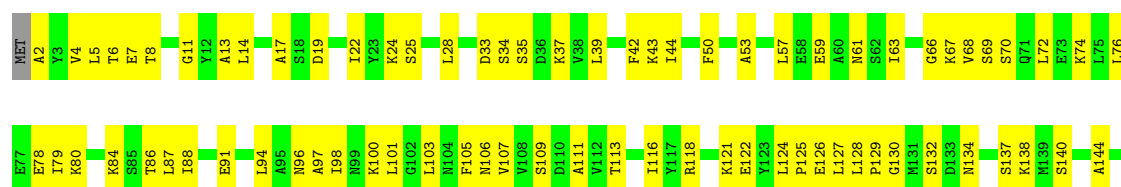
- Molecule 26: Nucleolar protein 56

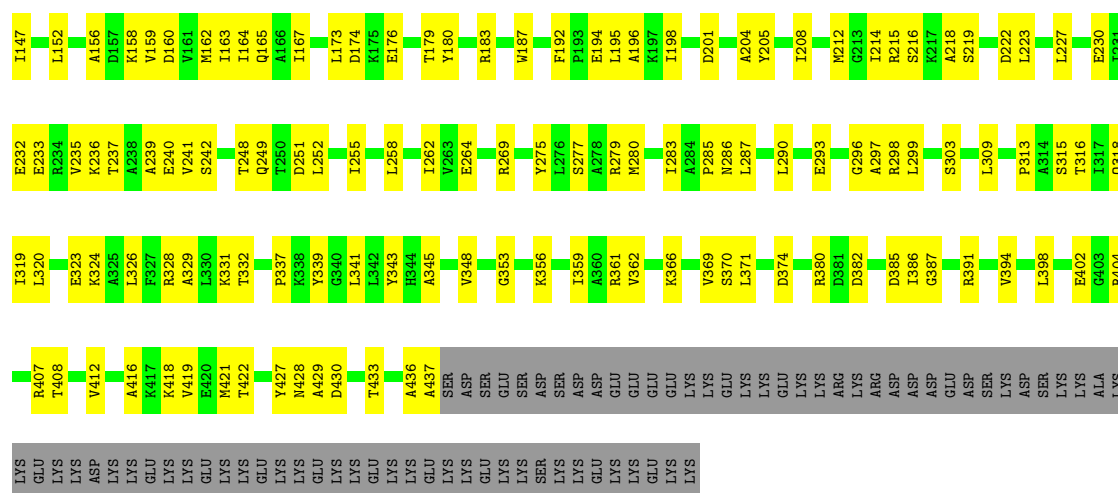
Chain CD:



- Molecule 27: Nucleolar protein 58

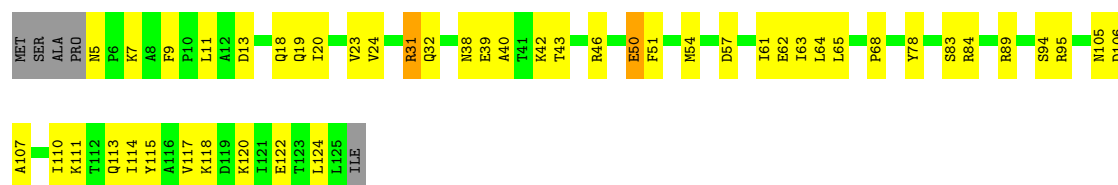
Chain CE: 





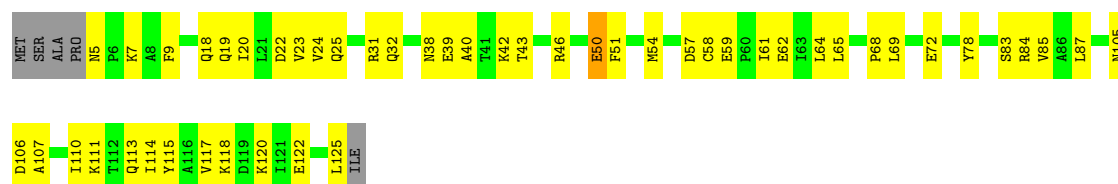
- Molecule 28: 13 kDa ribonucleoprotein-associated protein

Chain CF: 59% 36%



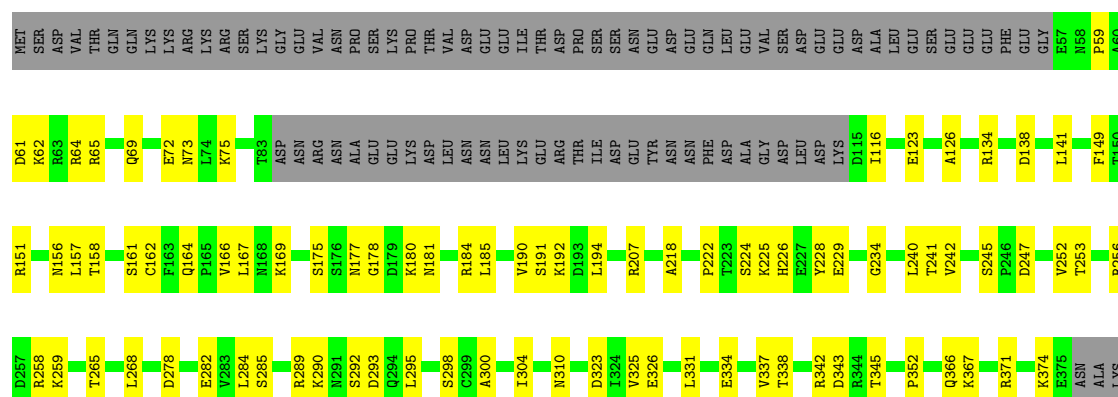
- Molecule 28: 13 kDa ribonucleoprotein-associated protein

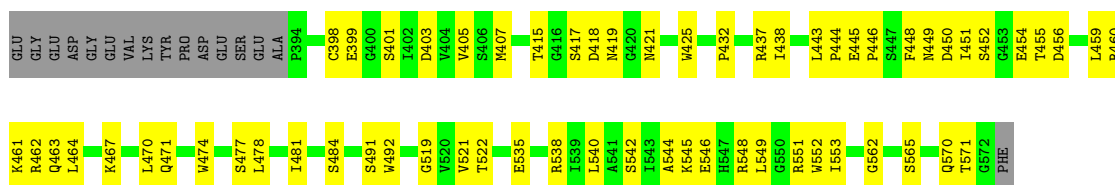
Chain CG: 57% 38%



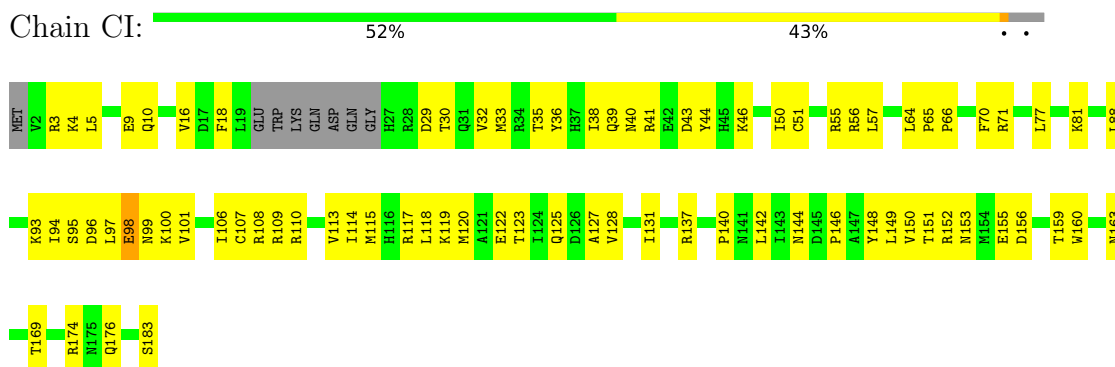
- Molecule 29: Ribosomal RNA-processing protein 9

Chain CH: 56% 26% 18%

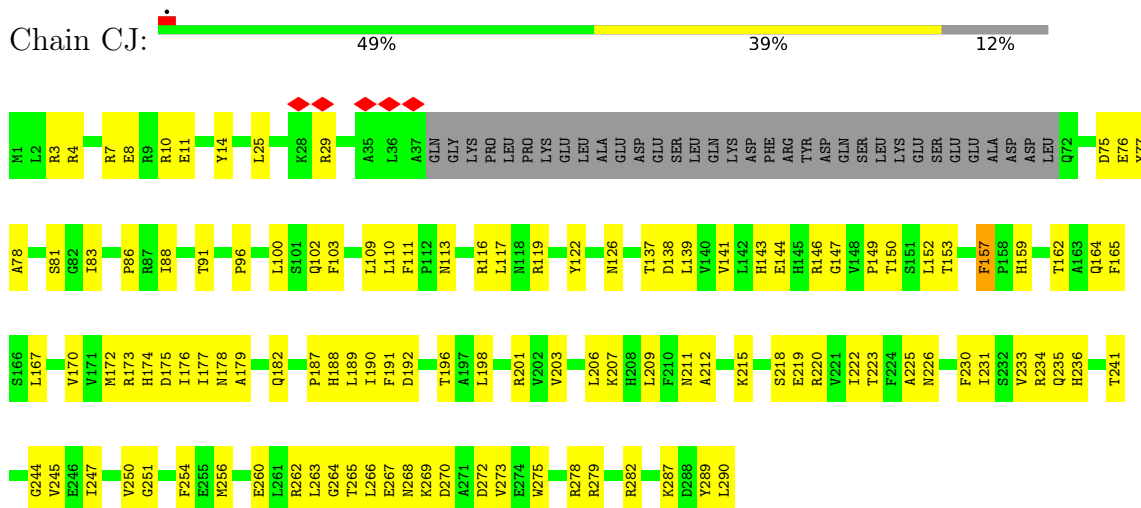




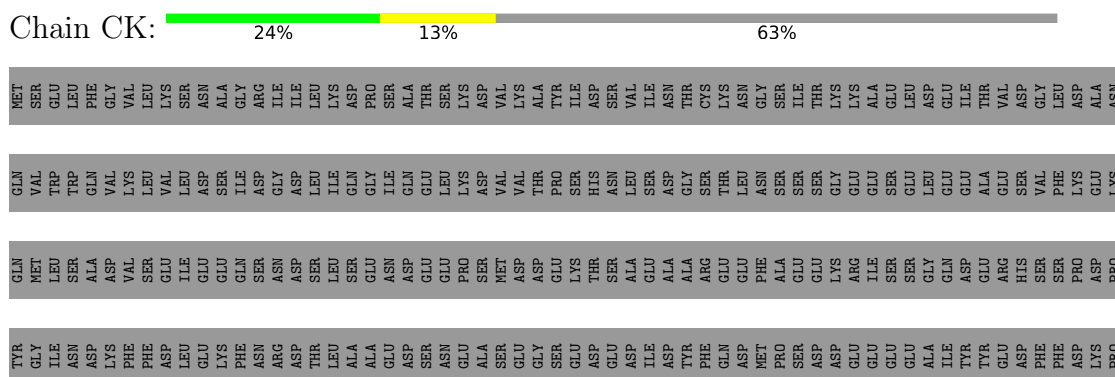
• Molecule 30: U3 small nucleolar ribonucleoprotein protein IMP3

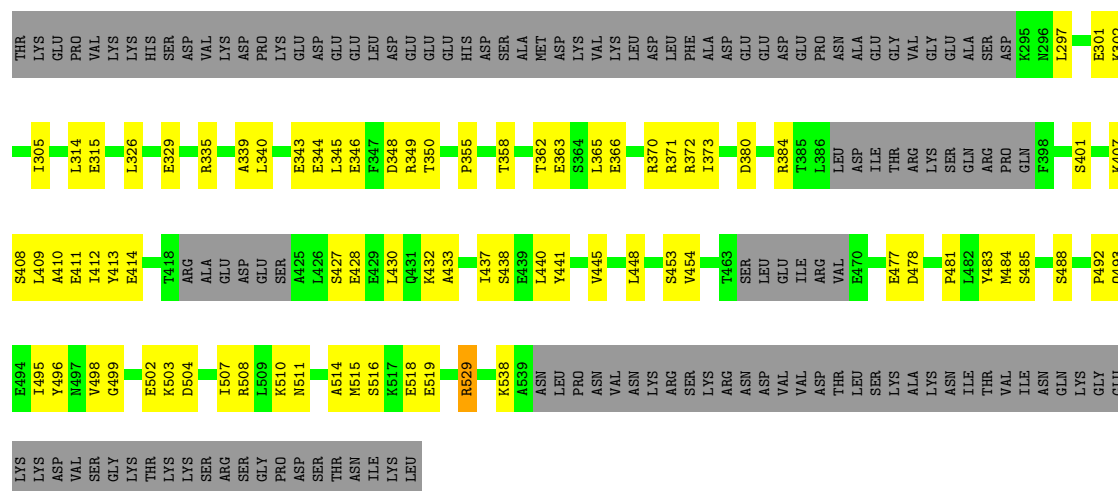


• Molecule 31: U3 small nucleolar ribonucleoprotein protein IMP4

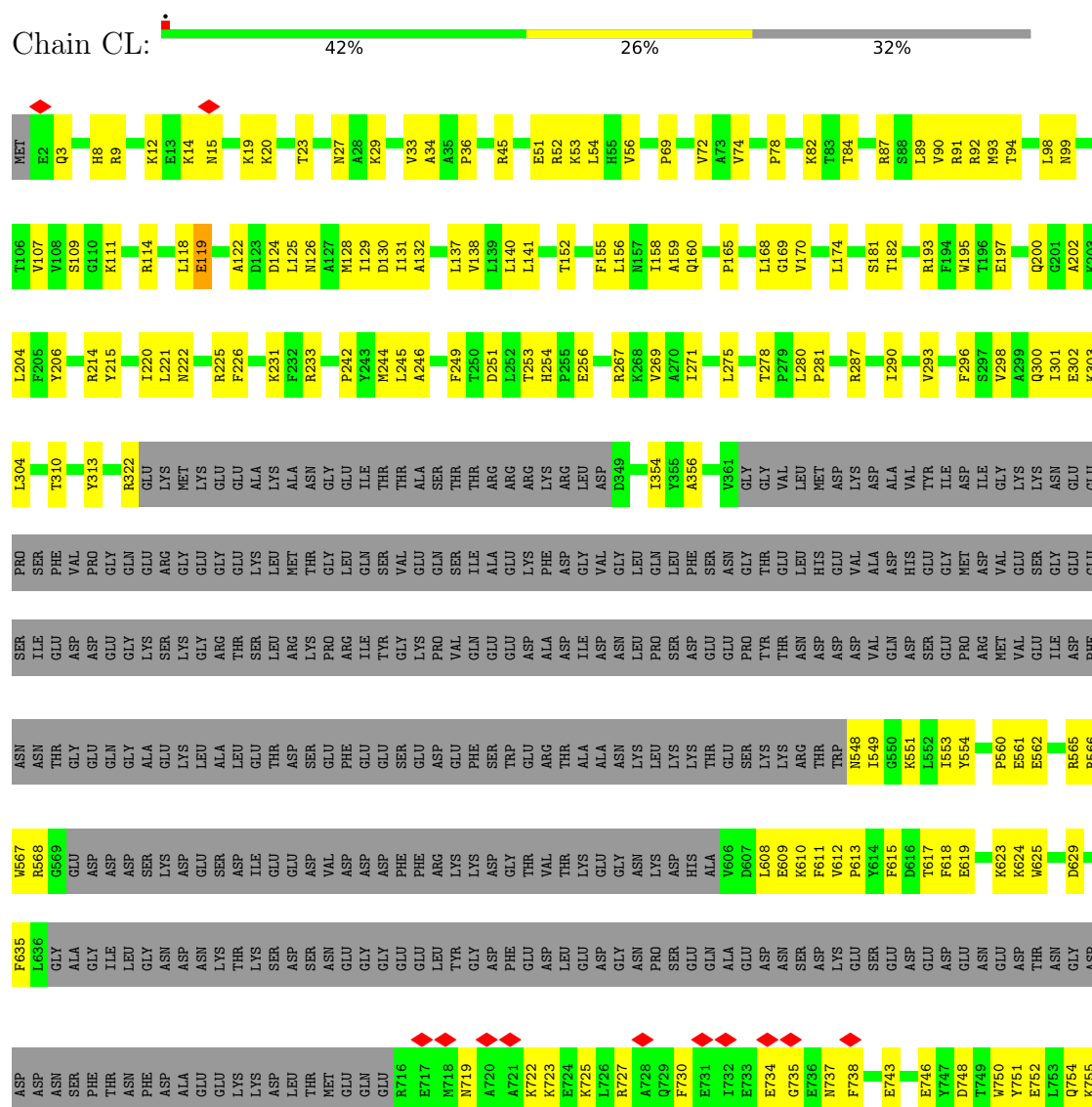


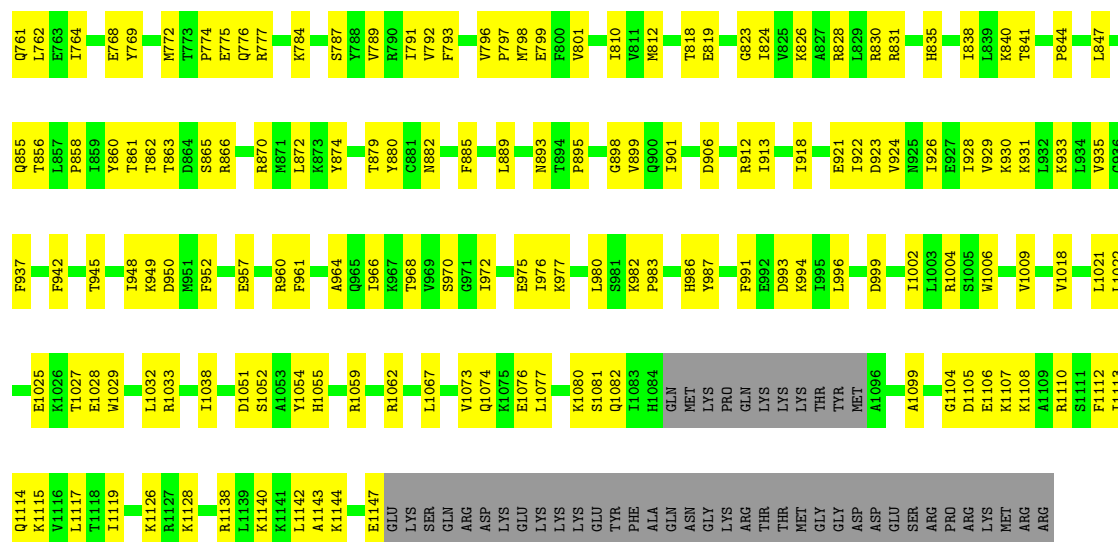
• Molecule 32: U3 small nucleolar RNA-associated protein MPP10





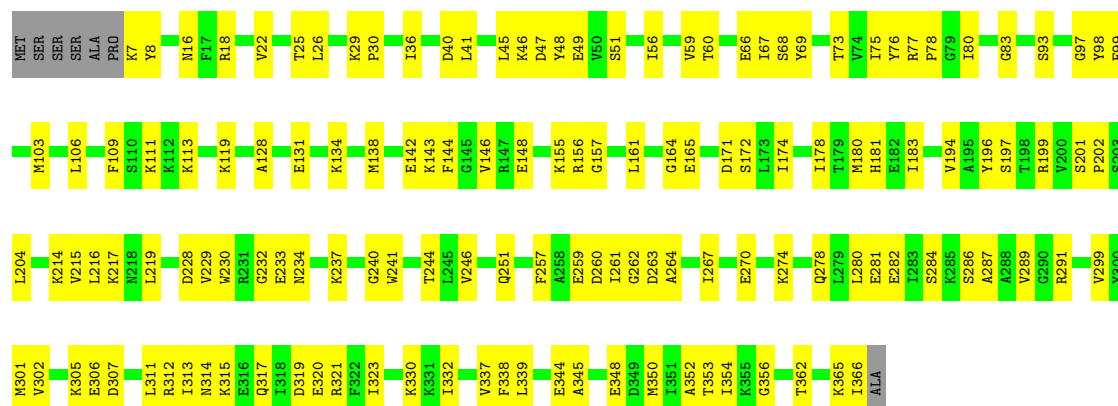
● Molecule 33: Ribosome biogenesis protein BMS1





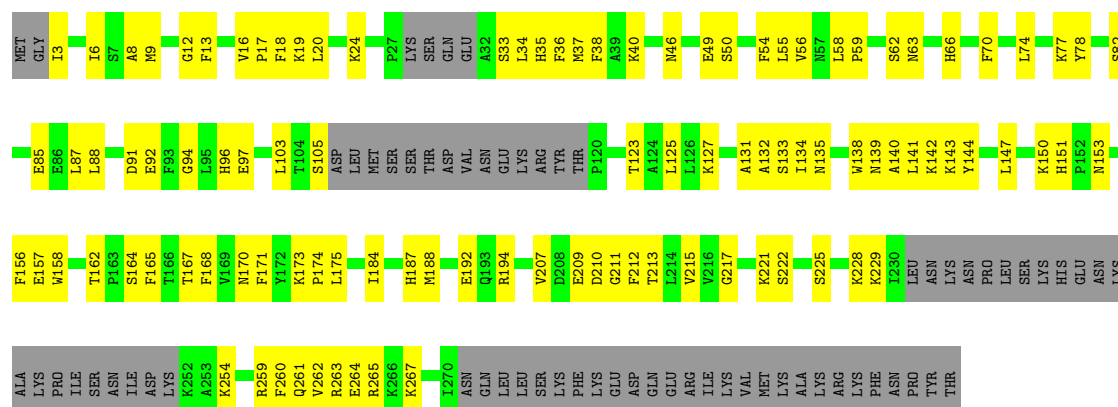
• Molecule 34: RNA 3'-terminal phosphate cyclase-like protein

Chain CM: 60% 38% .



• Molecule 35: Ribosomal RNA-processing protein 7

Chain CN: 42% 35% 23%

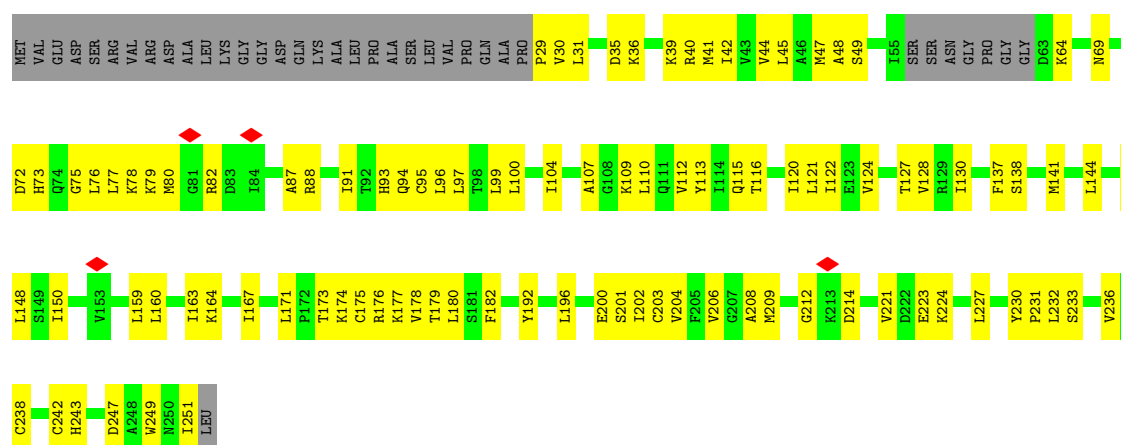


• Molecule 36: Probable ATP-dependent RNA helicase DHR1

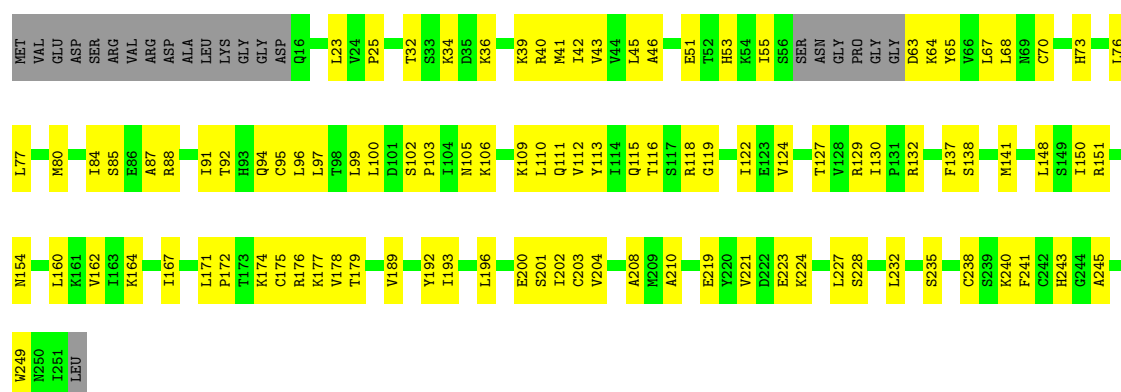




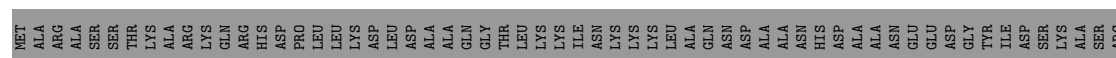
• Molecule 37: Ribosomal RNA small subunit methyltransferase NEP1



• Molecule 37: Ribosomal RNA small subunit methyltransferase NEP1

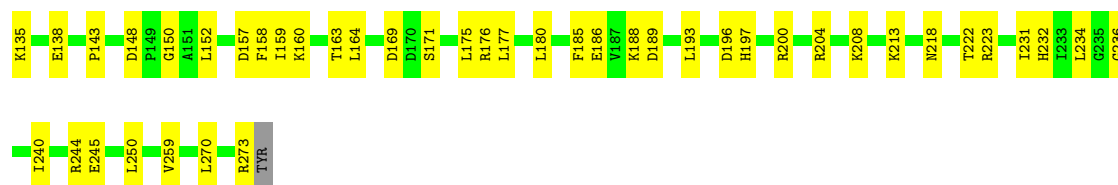


• Molecule 38: Essential nuclear protein 1



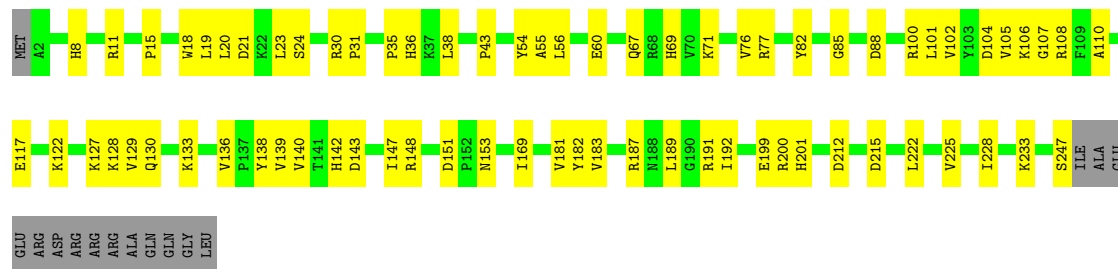


WORLDWIDE
PDB
PROTEIN DATA BANK



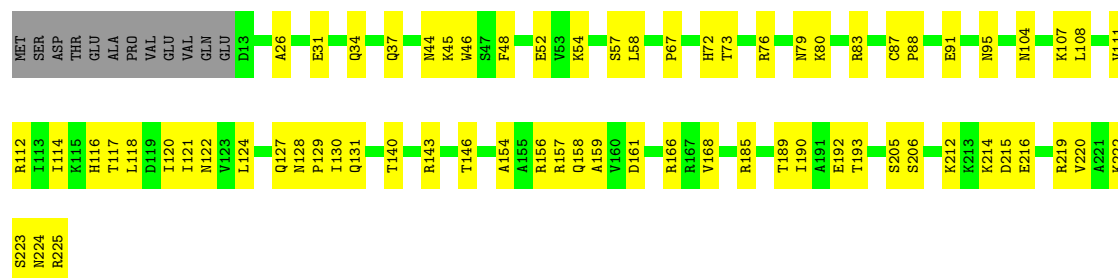
- Molecule 45: 40S ribosomal protein S4-A

Chain DE: 67% 27% 6%



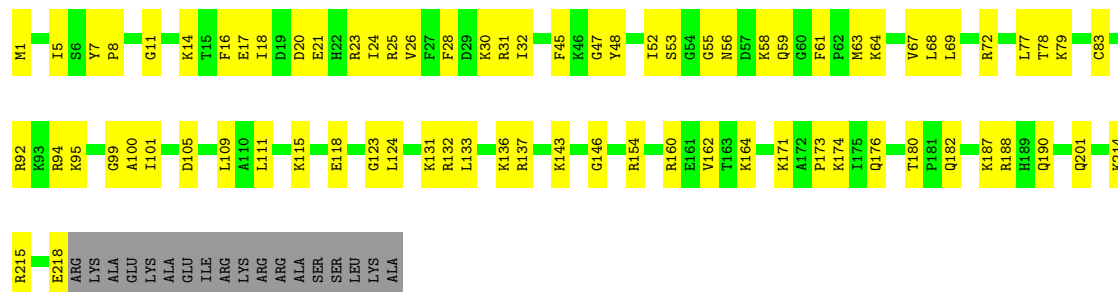
- Molecule 46: 40S ribosomal protein S5

Chain DF: 64% 31% 5%



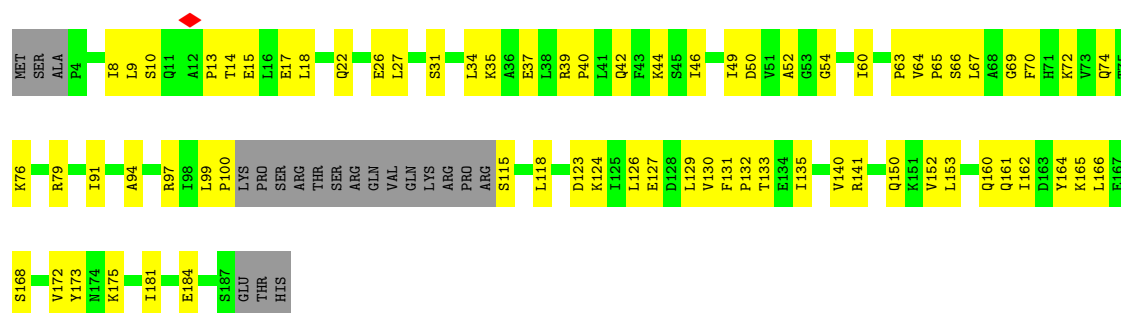
- Molecule 47: 40S ribosomal protein S6-A

Chain DG: 60% 32% 8%



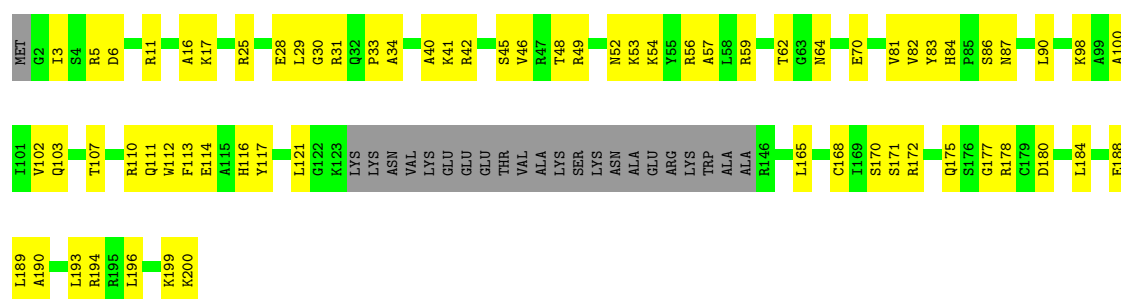
- Molecule 48: 40S ribosomal protein S7-A

Chain DH: 53% 37% 11%



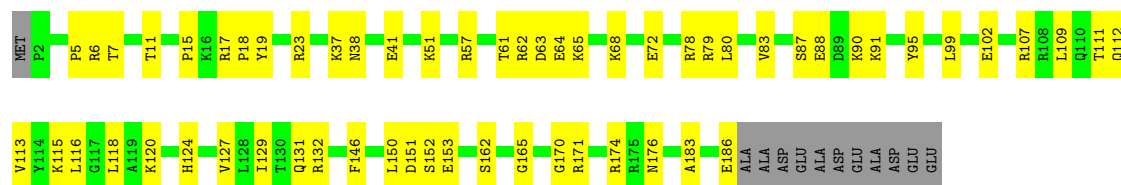
- Molecule 49: 40S ribosomal protein S8-A

Chain DI:



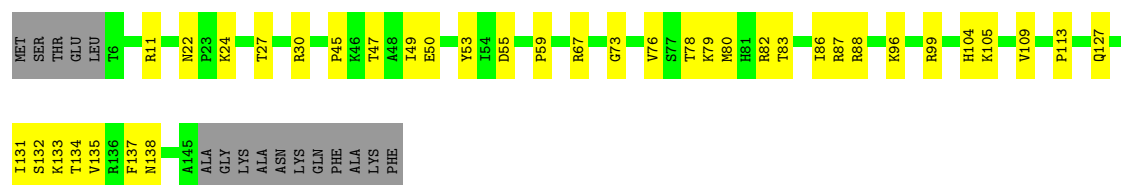
- Molecule 50: 40S ribosomal protein S9-A

Chain DJ:



- Molecule 51: 40S ribosomal protein S11-A

Chain DL:



- Molecule 52: 40S ribosomal protein S13

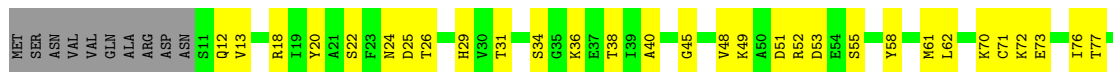
Chain DN:





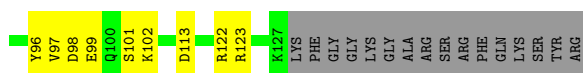
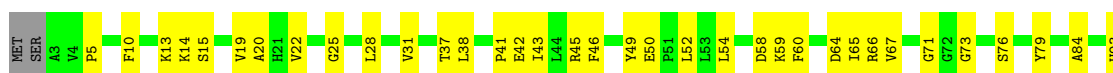
• Molecule 53: 40S ribosomal protein S14-A

Chain DO: 56% 36% 7%



• Molecule 54: 40S ribosomal protein S16-A

Chain DQ: 57% 31% 13%



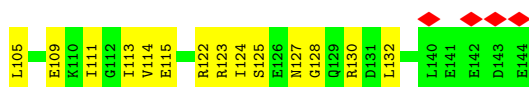
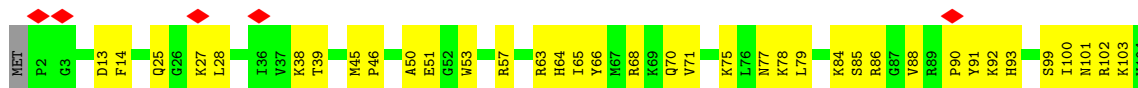
• Molecule 55: 40S ribosomal protein S18-A

Chain DS: 5% 40% 32% 28%



• Molecule 56: 40S ribosomal protein S19-A

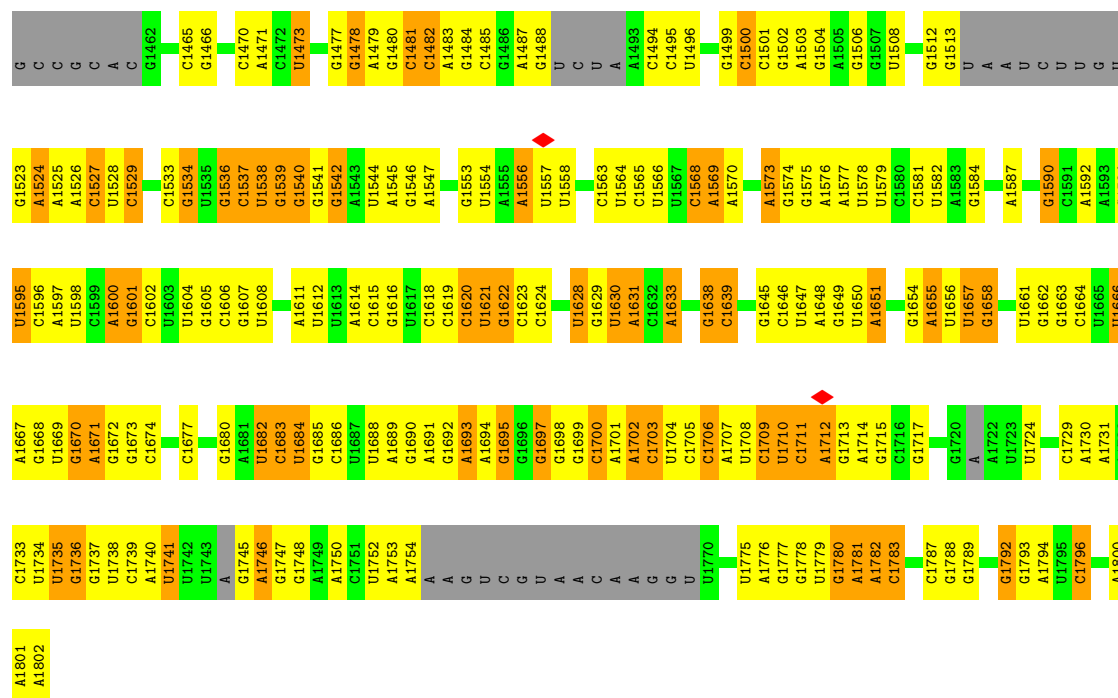
Chain DT: 6% 64% 35%



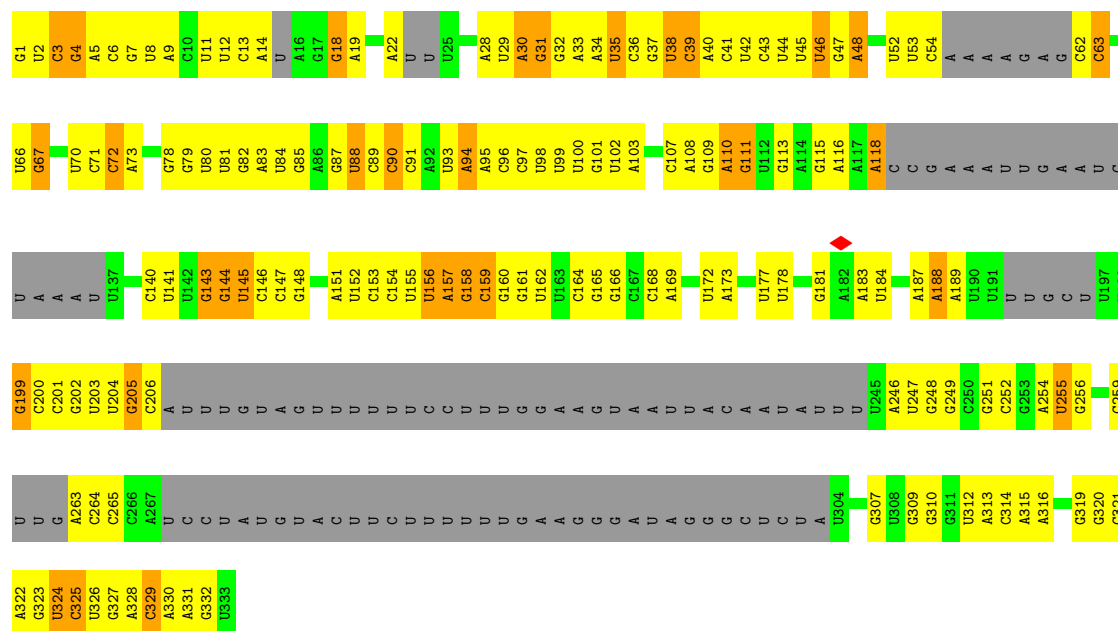
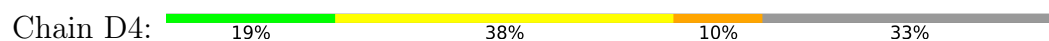
• Molecule 57: 40S ribosomal protein S22-A

Chain DW: 72% 28%

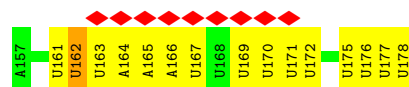




• Molecule 63: U3 snoRNA

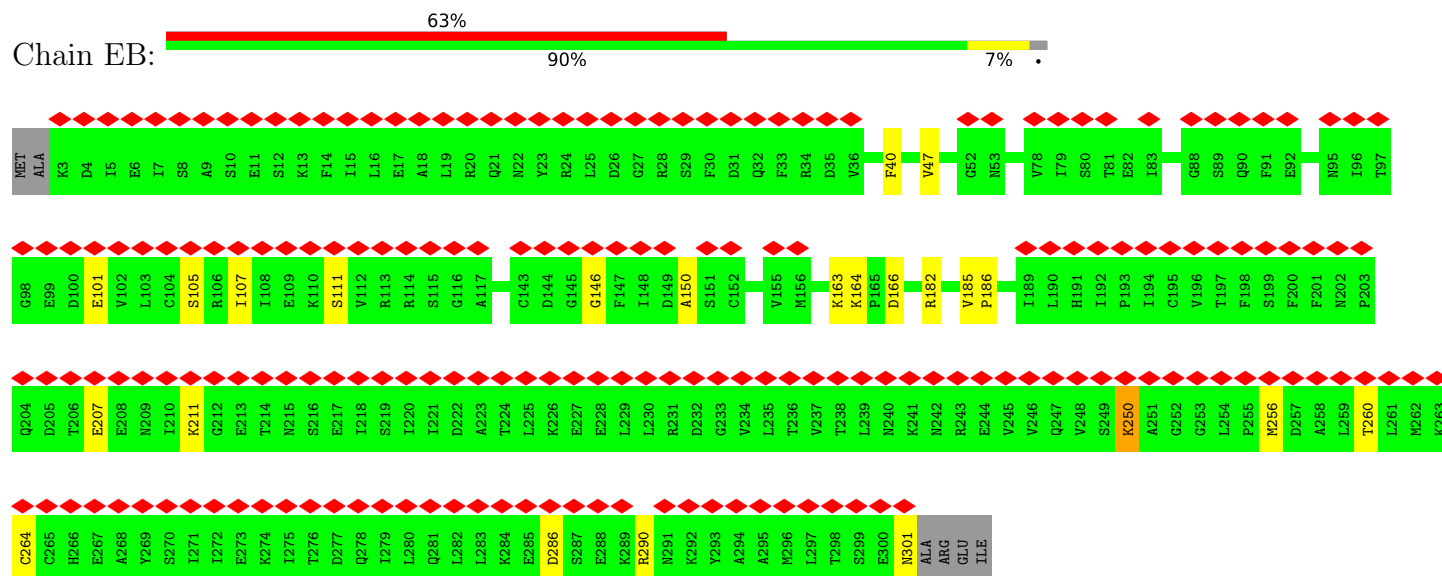


• Molecule 64: RNA



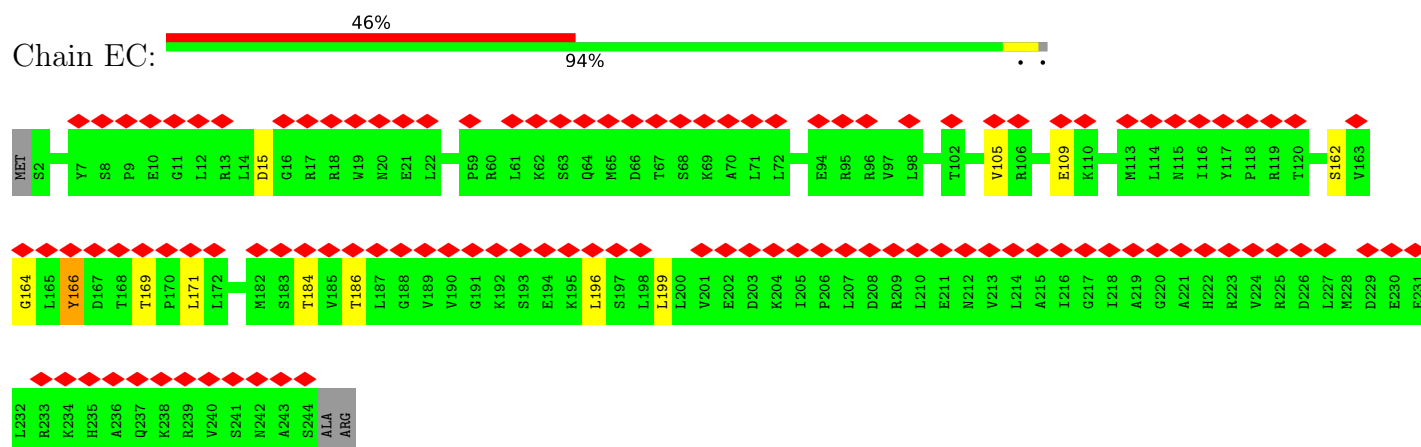
• Molecule 65: Exosome complex component RRP45

Chain EB:



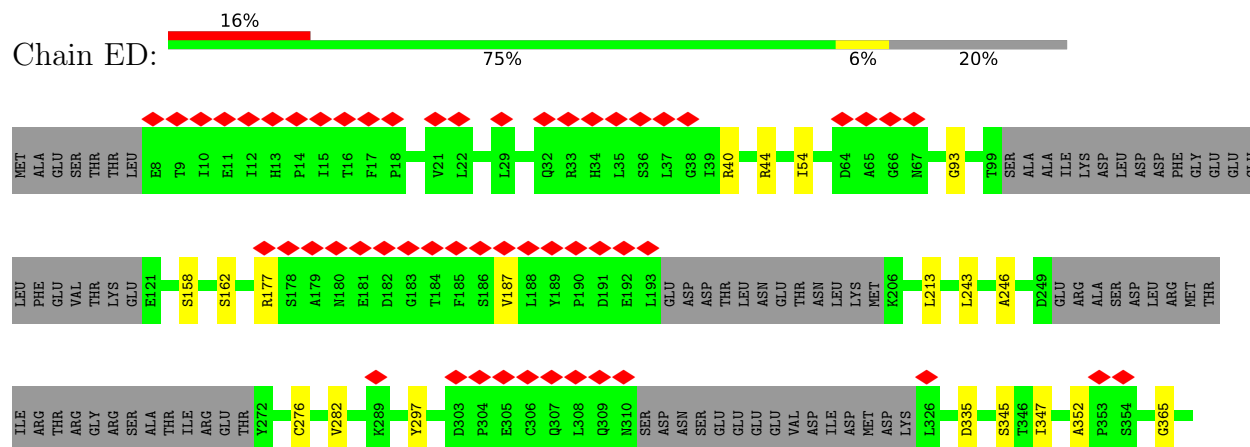
• Molecule 66: Exosome complex component SKI6

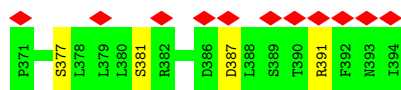
Chain EC:



• Molecule 67: Exosome complex component RRP43

Chain ED:

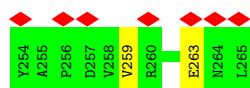
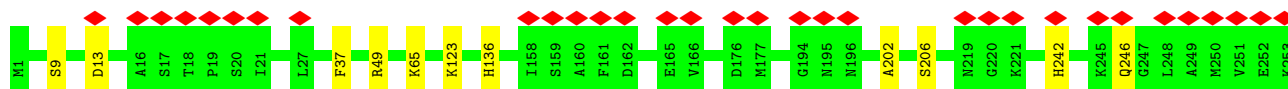




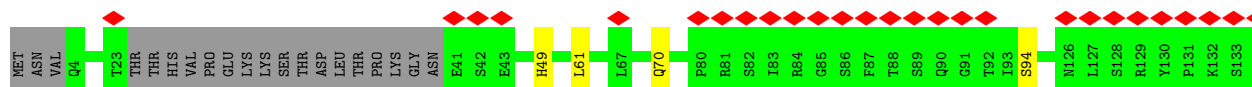
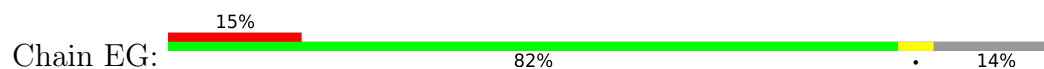
- Molecule 68: Exosome complex component RRP46



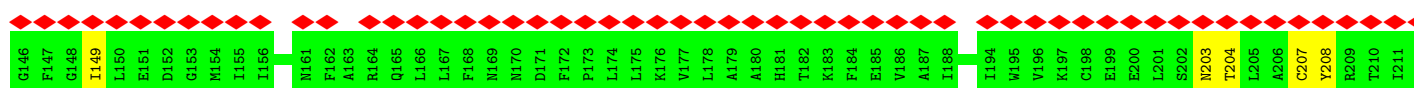
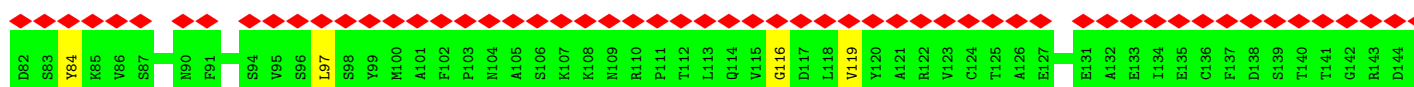
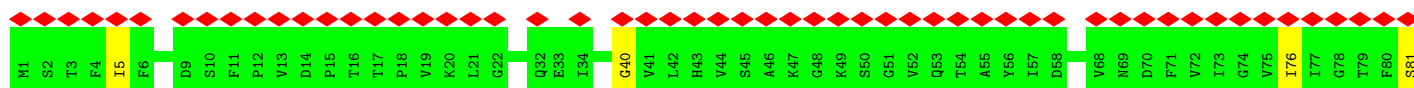
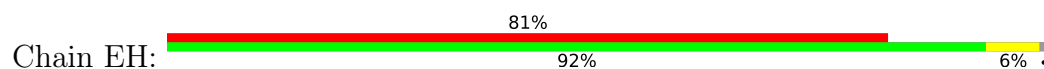
- Molecule 69: Exosome complex component RRP42

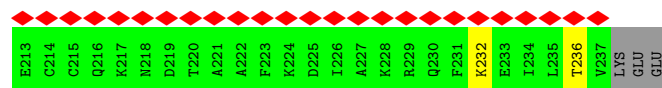


- Molecule 70: Exosome complex component MTR3

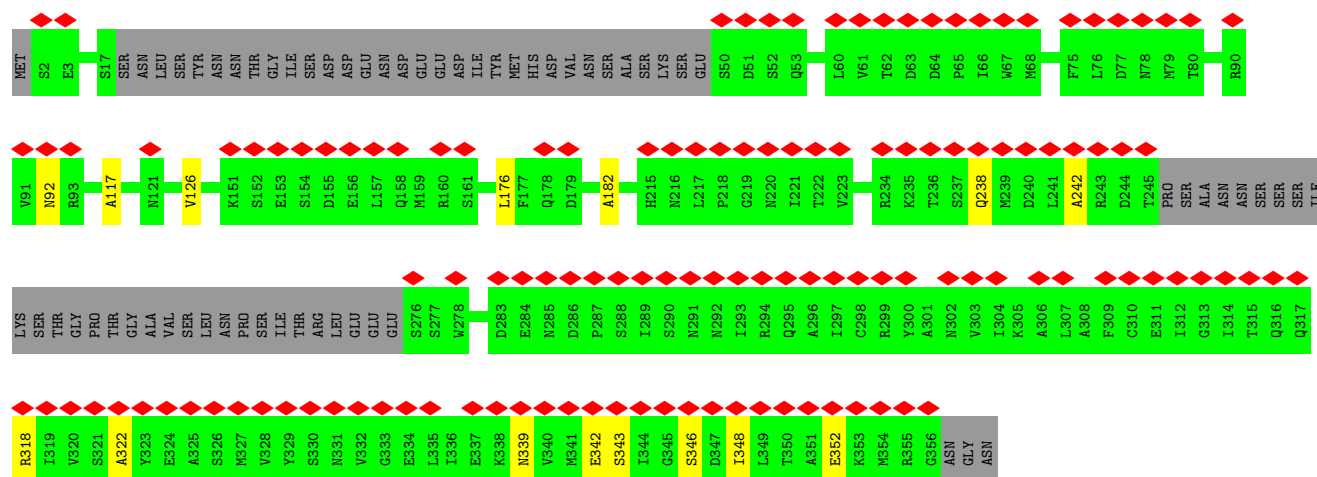
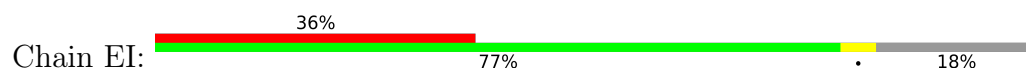


- Molecule 71: Exosome complex component RRP40

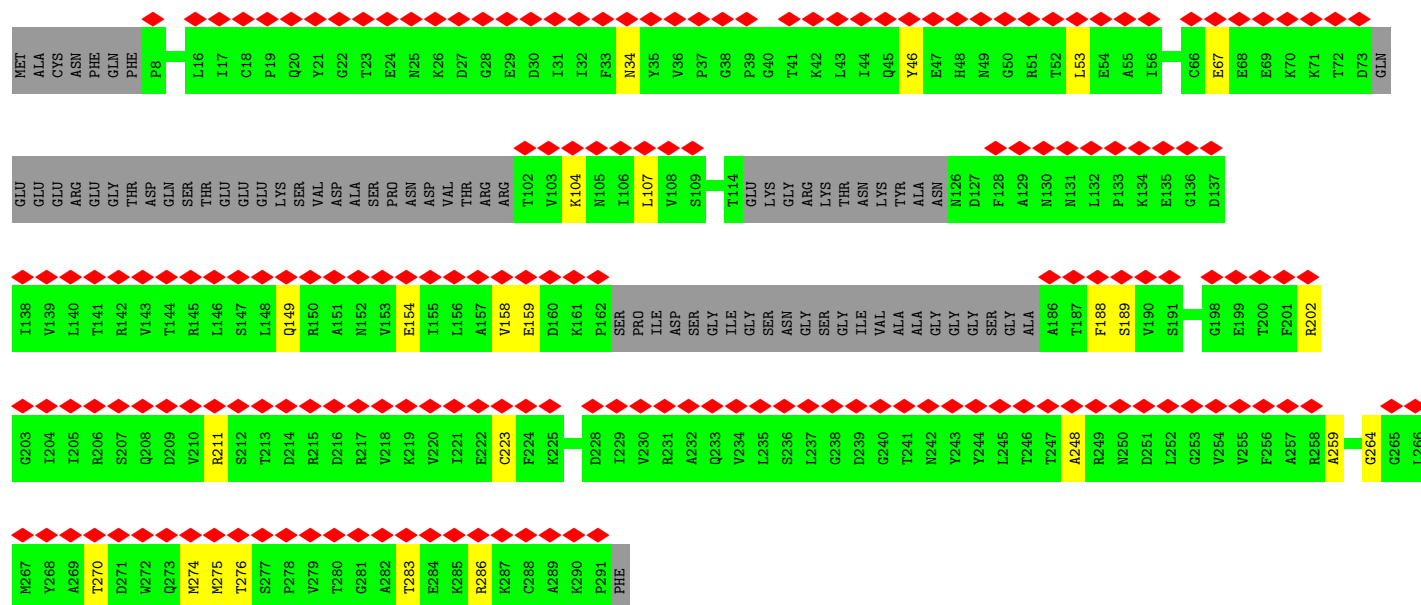




• Molecule 72: Exosome complex component RRP4

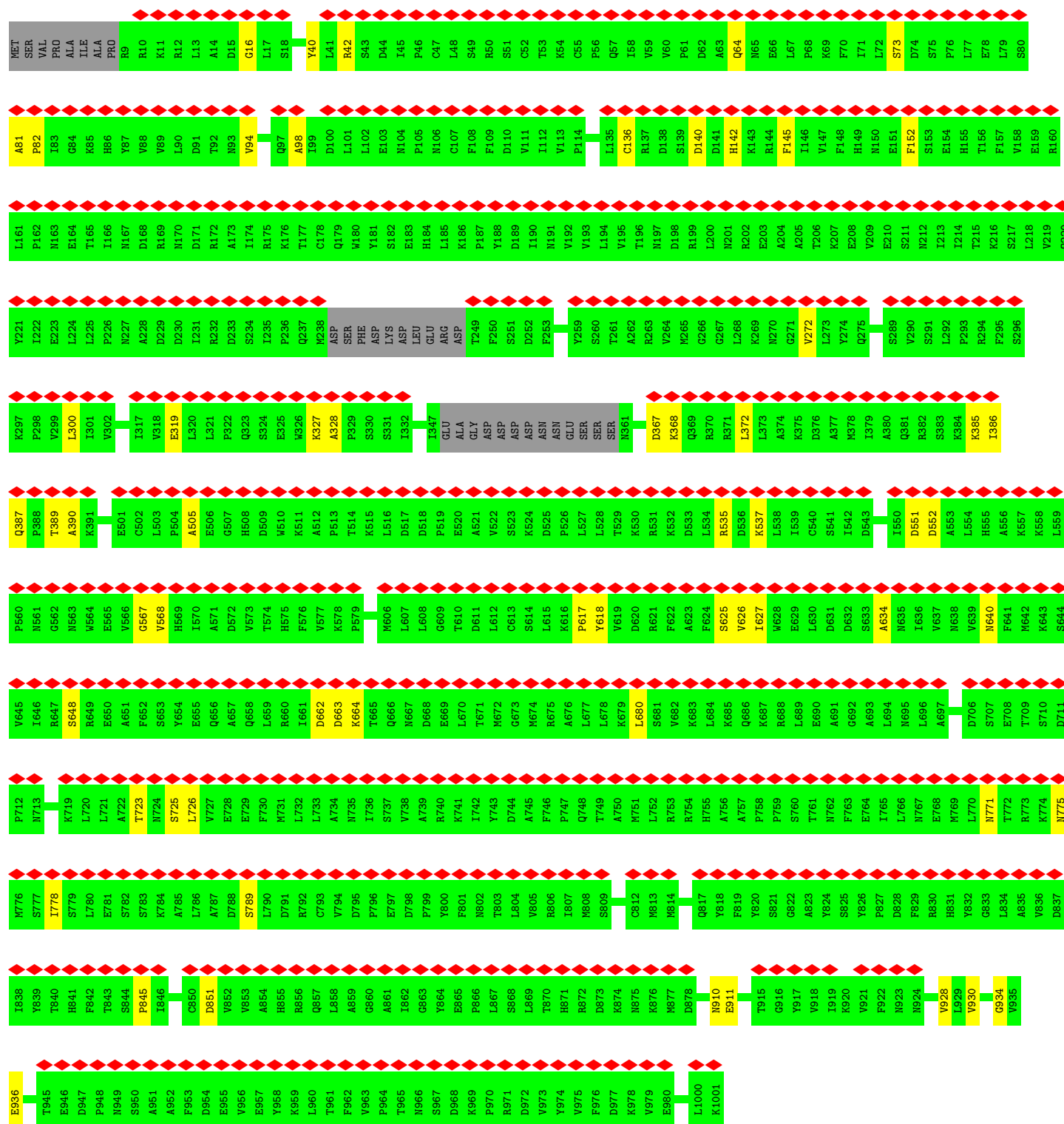


• Molecule 73: Exosome complex component CSL4

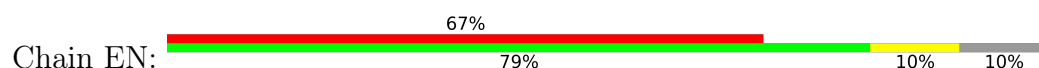


• Molecule 74: Exosome complex exonuclease DIS3





• Molecule 75: ATP-dependent RNA helicase DOB1



MET	ASP	SER	THR	ASP	LEU	PHE	ASP	VAL	PHE	GLU	GLU	THR	PRO	VAL	GLU	LEU	PRO	THR	ASP	SER	GLY	GLU	LYS	ASN	ALA	ASP	THR	VAL	GLY	ASP	THR	PRO	ASP	HIS	THR	GLN	ASP	LYS	LYS	HIS	GLY	LEU	GLU	GLU	GLU	HIS	GLU	GLU	ASN	SER	GLU	ASN	LYS
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Lys	Lys	Lys	Lys	Asn	Lys	Ser	Lys	Ser	Thr	Glu	Asp	Lys	Lys	Asn	Lys	Lys	Val	Val	Pro	Val	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Q1012	I1013	C1014	K1015	M1016	T1017	D1018	V1019	Y1020	E1021	G1022	R1026	E1032	V1035	K1036	E1037	L1038	V1039	A1042	N1043	G1046	M1047	S1048	S1049	L1050	K1051	E1052	K1053	M1054	E1055	A1056	V1057	L1058	K1059	L1060	I1061	H1062	R1063	D1064	I1065	V1066	S1067	A1068	G1069	S1070	L1071	Y1072	L1073
-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	35320	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.473	Depositor
Minimum map value	-0.263	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	571.86, 571.86, 571.86	wwPDB
Map dimensions	540, 540, 540	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, MG, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	CA	0.71	0/1917	0.73	0/2588
1	CB	0.30	0/1815	0.53	1/2448 (0.0%)
2	DA	0.60	0/1937	0.66	0/2593
3	UA	0.59	1/6465 (0.0%)	0.67	1/8752 (0.0%)
4	UB	0.20	0/4158	0.43	0/5607
5	UC	0.63	0/699	0.68	0/919
6	UD	0.24	0/5369	0.51	0/7272
7	UE	0.34	0/3840	0.52	0/5208
8	UF	0.46	0/2538	0.60	1/3405 (0.0%)
9	UG	0.60	0/3796	0.73	2/5126 (0.0%)
10	UH	0.17	0/2773	0.50	0/3798
11	UI	0.16	0/735	0.44	0/987
12	UJ	0.35	0/9111	0.55	3/12323 (0.0%)
13	UK	0.29	0/1869	0.58	0/2472
14	UL	0.38	0/6324	0.58	0/8546
15	UM	0.39	0/6071	0.60	2/8218 (0.0%)
16	UN	0.50	0/1697	0.65	1/2284 (0.0%)
17	UO	0.23	0/3993	0.53	0/5413
18	UP	0.26	0/499	0.55	0/659
19	UQ	0.21	0/6688	0.45	1/9062 (0.0%)
20	UR	0.40	0/3875	0.57	0/5254
21	US	0.15	0/3667	0.41	0/5001
22	UT	0.46	0/19132	0.65	1/25831 (0.0%)
23	UU	0.49	0/7059	0.58	0/9536
24	UV	0.32	0/8962	0.49	0/12120
25	UX	0.74	0/1353	0.80	2/1819 (0.1%)
26	CD	0.51	0/3041	0.60	0/4098
27	CE	0.34	0/3364	0.55	0/4539
28	CF	0.66	0/928	0.89	4/1262 (0.3%)
28	CG	0.66	0/928	0.88	4/1262 (0.3%)
29	CH	0.55	0/3809	0.64	0/5128
30	CI	0.41	0/1494	0.64	2/2008 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	CJ	0.49	0/2118	0.67	1/2855 (0.0%)
32	CK	0.44	0/1808	0.63	2/2424 (0.1%)
33	CL	0.54	0/6691	0.65	2/9000 (0.0%)
34	CM	0.46	0/2832	0.58	0/3825
35	CN	0.32	0/1909	0.49	0/2571
36	JD	0.26	0/6634	0.54	0/8927
37	JF	0.14	0/1727	0.42	0/2329
37	JG	0.19	0/1828	0.45	0/2470
38	JH	0.10	0/1293	0.36	0/1801
39	JI	0.12	0/1313	0.36	0/1830
40	JL	0.25	0/2305	0.51	0/3116
41	JM	0.33	0/1151	0.62	0/1535
42	JP	0.80	1/3844 (0.0%)	0.80	3/5174 (0.1%)
43	Db	0.61	0/620	0.63	0/838
44	JJ	0.54	0/1600	0.68	0/2154
45	DE	0.83	0/1991	0.76	0/2683
46	DF	0.47	0/1690	0.61	0/2285
47	DG	0.49	0/1779	0.62	0/2379
48	DH	0.51	0/1383	0.69	0/1863
49	DI	0.64	0/1422	0.69	0/1899
50	DJ	0.79	0/1519	0.75	0/2035
51	DL	0.72	0/1155	0.66	0/1557
52	DN	0.59	0/1215	0.65	0/1638
53	DO	0.59	0/933	0.72	0/1256
54	DQ	0.51	0/986	0.59	0/1330
55	DS	0.21	0/871	0.60	0/1171
56	DT	0.30	0/1130	0.62	0/1517
57	DW	0.87	0/1038	0.78	0/1395
58	DX	0.62	0/1133	0.73	0/1510
59	DY	0.69	0/1087	0.68	0/1449
60	Dc	0.54	0/499	0.63	0/670
61	D2	0.16	0/1946	0.27	0/3024
62	D3	0.60	0/33586	0.44	2/52290 (0.0%)
63	D4	0.32	0/5263	0.32	0/8171
64	EA	0.42	0/405	0.72	0/625
65	EB	0.60	1/1474 (0.1%)	0.79	0/2050
66	EC	0.60	0/1198	0.79	0/1666
67	ED	0.54	0/1569	0.82	0/2179
68	EE	0.57	0/1109	0.81	0/1545
69	EF	0.52	0/1319	0.80	0/1839
70	EG	0.56	0/1055	0.80	0/1462
71	EH	0.55	0/1169	0.86	2/1626 (0.1%)
72	EI	0.55	0/1437	0.84	0/1992

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
73	EJ	0.48	0/1087	0.84	0/1504
74	EK	0.66	0/4818	1.10	10/6720 (0.1%)
75	EN	0.49	0/4760	0.84	4/6629 (0.1%)
All	All	0.48	3/249605 (0.0%)	0.60	51/346346 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	DA	0	1
9	UG	0	2
10	UH	0	3
14	UL	0	1
15	UM	0	1
17	UO	0	1
22	UT	0	2
25	UX	0	1
26	CD	0	1
36	JD	0	1
42	JP	0	2
44	JJ	0	1
51	DL	0	1
59	DY	0	1
66	EC	0	1
67	ED	0	3
68	EE	0	1
69	EF	0	1
70	EG	0	2
72	EI	0	1
73	EJ	0	1
75	EN	0	3
All	All	0	32

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	JP	35	PHE	CA-CB	-7.71	1.42	1.53
65	EB	250	LYS	CA-CB	-7.15	1.43	1.53
3	UA	493	TRP	CA-C	-6.96	1.43	1.52

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
74	EK	272	VAL	N-CA-C	9.35	120.16	110.62
62	D3	849	C	OP2-P-O3'	-9.11	80.68	108.00
28	CG	31	ARG	CA-CB-CG	-8.68	96.74	114.10
28	CF	31	ARG	CA-CB-CG	-8.66	96.77	114.10
62	D3	849	C	OP1-P-O3'	-8.04	83.88	108.00

There are no chirality outliers.

5 of 32 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	DA	11	LYS	Peptide
9	UG	199	LEU	Peptide
9	UG	452	VAL	Peptide
10	UH	266	ILE	Peptide
10	UH	74	ILE	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CA	1881	0	1928	113	0
1	CB	1782	0	1826	109	0
2	DA	1912	0	2023	89	0
3	UA	6322	0	6223	250	0
4	UB	4105	0	3846	155	0
5	UC	694	0	742	31	0
6	UD	5269	0	5281	278	0
7	UE	3772	0	3806	197	0
8	UF	2487	0	2533	105	0
9	UG	3718	0	3721	148	0
10	UH	2771	0	1817	79	0
11	UI	723	0	770	38	0
12	UJ	8961	0	9273	386	0
13	UK	1845	0	1926	104	0
14	UL	6199	0	6221	319	0
15	UM	5970	0	6009	373	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	UN	1667	0	1658	71	0
17	UO	3911	0	3906	292	0
18	UP	495	0	561	41	0
19	UQ	6557	0	6489	346	0
20	UR	3791	0	3772	206	0
21	US	3587	0	3200	138	0
22	UT	18789	0	19126	922	0
23	UU	6922	0	6886	313	0
24	UV	8753	0	8867	428	0
25	UX	1330	0	1416	61	0
26	CD	2994	0	3018	106	0
27	CE	3326	0	3406	176	0
28	CF	916	0	964	56	0
28	CG	916	0	964	53	0
29	CH	3736	0	3756	120	0
30	CI	1468	0	1519	77	0
31	CJ	2081	0	2112	109	0
32	CK	1789	0	1801	102	0
33	CL	6551	0	6707	289	0
34	CM	2781	0	2878	113	0
35	CN	1868	0	1845	98	0
36	JD	6509	0	6724	372	0
37	JF	1701	0	1767	82	0
37	JG	1799	0	1872	94	0
38	JH	1295	0	570	3	0
39	JI	1314	0	610	5	0
40	JL	2262	0	2330	93	0
41	JM	1131	0	1161	63	0
42	JP	3765	0	3714	154	0
43	Db	610	0	630	16	0
44	JJ	1573	0	1650	70	0
45	DE	1950	0	2035	57	0
46	DF	1669	0	1724	58	0
47	DG	1755	0	1846	73	0
48	DH	1361	0	1437	54	0
49	DI	1399	0	1431	60	0
50	DJ	1494	0	1573	46	0
51	DL	1129	0	1196	31	0
52	DN	1192	0	1255	34	0
53	DO	922	0	946	45	0
54	DQ	969	0	1025	40	0
55	DS	861	0	896	39	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	DT	1112	0	1124	41	0
57	DW	1021	0	1060	36	0
58	DX	1115	0	1191	53	0
59	DY	1073	0	1132	24	0
60	Dc	497	0	535	23	0
61	D2	1741	0	876	50	0
62	D3	30042	0	15140	753	0
63	D4	4720	0	2397	159	0
64	EA	366	0	184	1	0
65	EB	1475	0	658	14	0
66	EC	1199	0	527	9	0
67	ED	1571	0	699	10	0
68	EE	1107	0	499	7	0
69	EF	1317	0	575	6	0
70	EG	1058	0	478	4	0
71	EH	1170	0	528	7	0
72	EI	1440	0	648	7	0
73	EJ	1091	0	500	12	0
74	EK	4818	0	2108	34	0
75	EN	4762	0	2107	58	0
76	Db	1	0	0	0	0
76	EK	1	0	0	0	0
76	UX	1	0	0	0	0
77	CL	32	0	12	3	0
78	CL	1	0	0	0	0
78	EK	1	0	0	0	0
All	All	242031	0	212166	8705	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 20.

The worst 5 of 8705 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:UL:671:PHE:HA	14:UL:684:TRP:O	1.25	1.32
3:UA:77:GLY:HA3	3:UA:95:PHE:O	1.27	1.28
9:UG:132:GLY:HA3	9:UG:150:LEU:O	1.33	1.24
23:UU:228:GLY:HA3	23:UU:246:ILE:O	1.12	1.22
59:DY:29:HIS:O	59:DY:67:GLY:HA2	1.36	1.21

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
61	D2	76/81 (93%)	23 (30%)	0
62	D3	1387/1802 (76%)	387 (27%)	25 (1%)
63	D4	214/333 (64%)	58 (27%)	4 (1%)
64	EA	21/22 (95%)	15 (71%)	0
All	All	1698/2238 (75%)	483 (28%)	29 (1%)

5 of 483 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
61	D2	6	A
61	D2	8	A
61	D2	11	A
61	D2	14	U
61	D2	15	G

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
62	D3	1058	U
63	D4	156	U
62	D3	1115	U
62	D3	1670	G
62	D3	1096	C

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 5 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
77	GTP	CL	2001	78	33,34,34	0.98	2 (6%)	50,54,54	1.66	10 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
77	GTP	CL	2001	78	-	7/22/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
77	CL	2001	GTP	C5-N7	-2.45	1.34	1.39
77	CL	2001	GTP	O4'-C4'	-2.10	1.40	1.45

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
77	CL	2001	GTP	C5-C4-N3	-5.02	120.39	128.39
77	CL	2001	GTP	C2-N3-C4	4.29	119.69	112.30
77	CL	2001	GTP	C2-N1-C6	-3.44	118.87	125.11
77	CL	2001	GTP	N9-C4-N3	3.09	132.13	125.95
77	CL	2001	GTP	C5-C6-N1	2.68	120.08	113.25

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

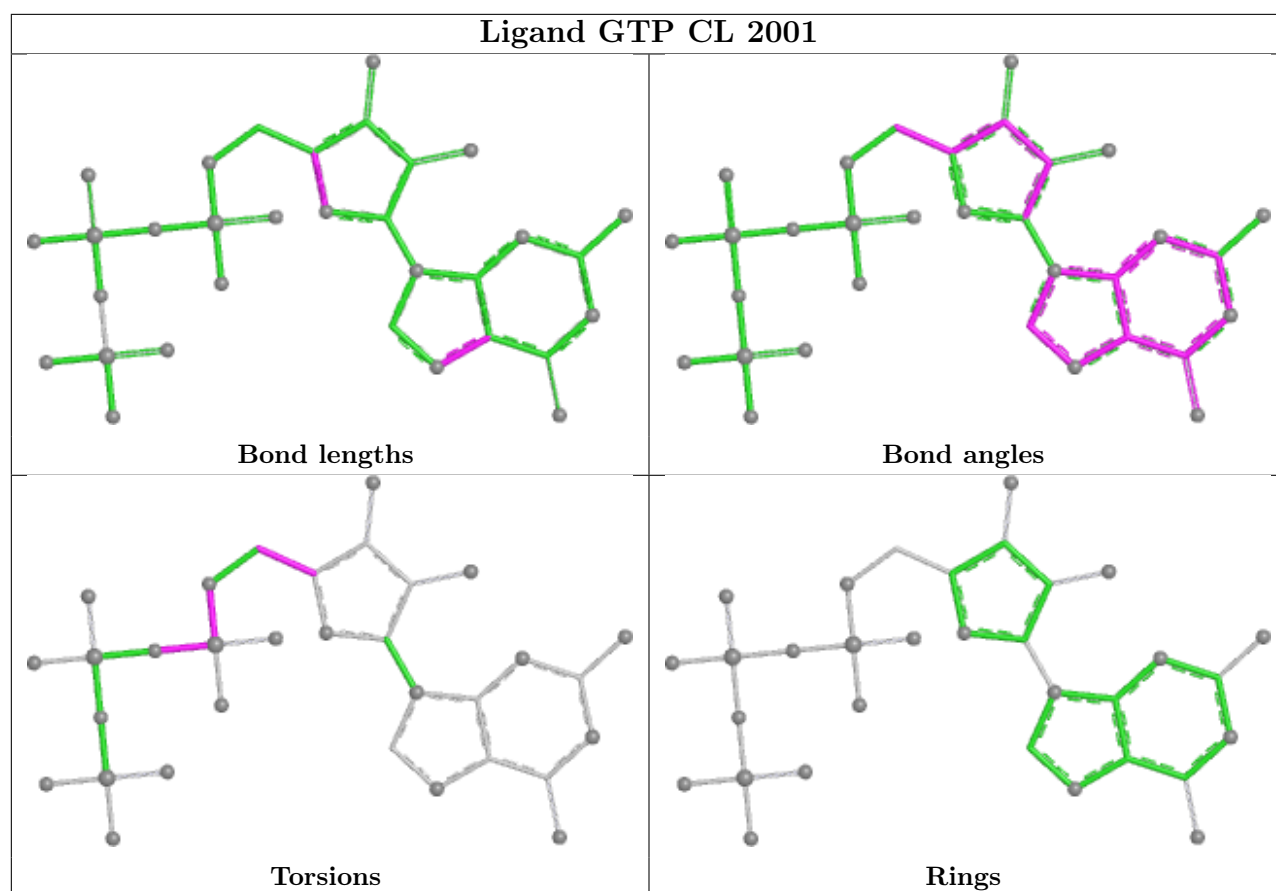
Mol	Chain	Res	Type	Atoms
77	CL	2001	GTP	C5'-O5'-PA-O3A
77	CL	2001	GTP	C5'-O5'-PA-O1A
77	CL	2001	GTP	C5'-O5'-PA-O2A
77	CL	2001	GTP	C3'-C4'-C5'-O5'
77	CL	2001	GTP	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
77	CL	2001	GTP	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
61	D2	4

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D2	92:C	O3'	281:G	P	62.30
1	D2	292:A	O3'	463:A	P	45.10
1	D2	70:A	O3'	80:A	P	19.53
1	D2	24:U	O3'	56:G	P	14.66

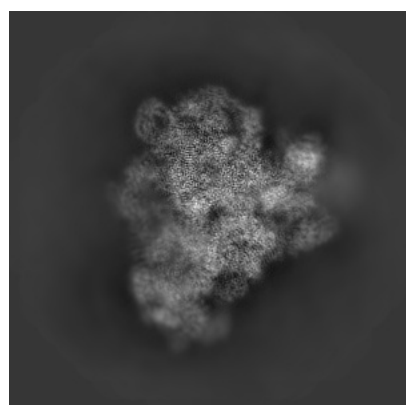
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11808. These allow visual inspection of the internal detail of the map and identification of artifacts.

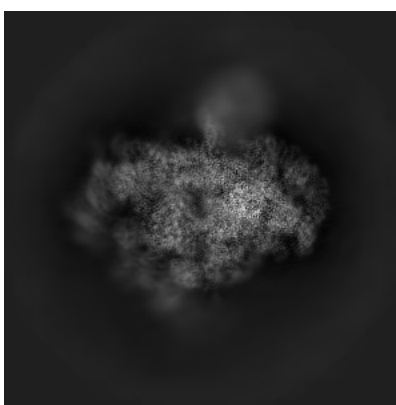
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

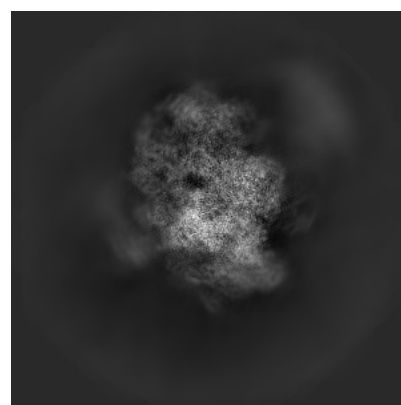
6.1.1 Primary map



X



Y

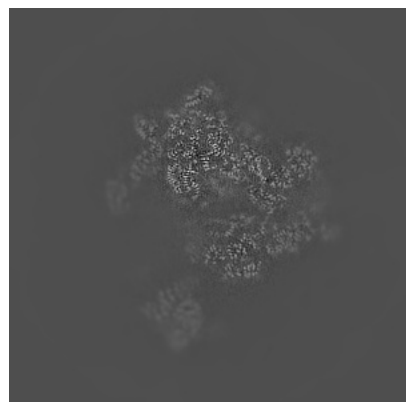


Z

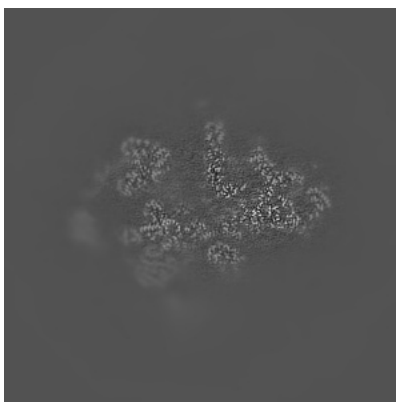
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

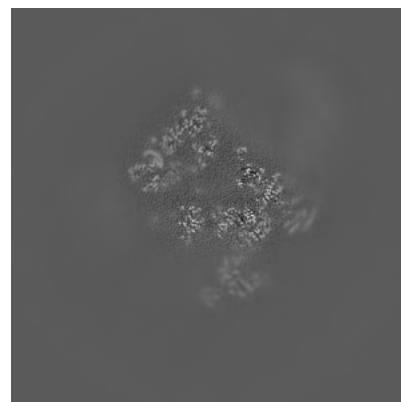
6.2.1 Primary map



X Index: 270



Y Index: 270

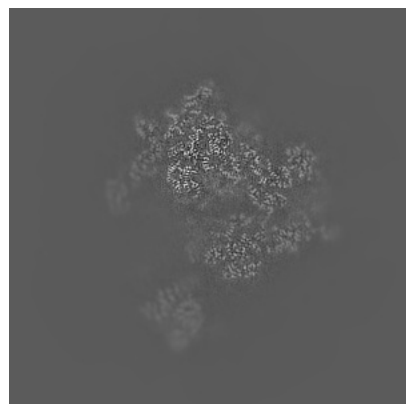


Z Index: 270

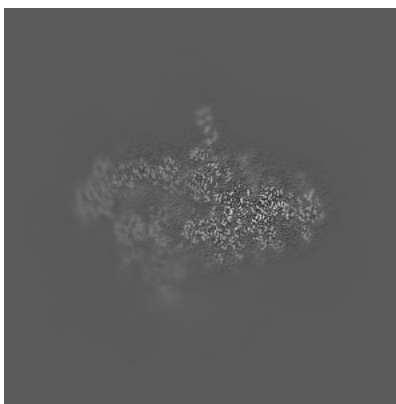
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

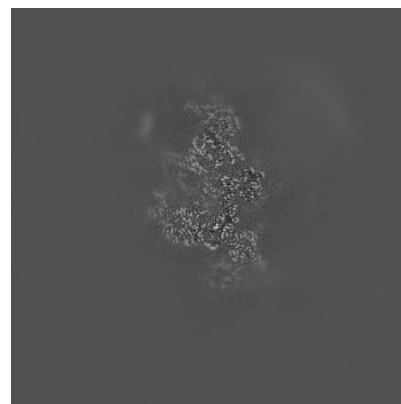
6.3.1 Primary map



X Index: 271



Y Index: 249

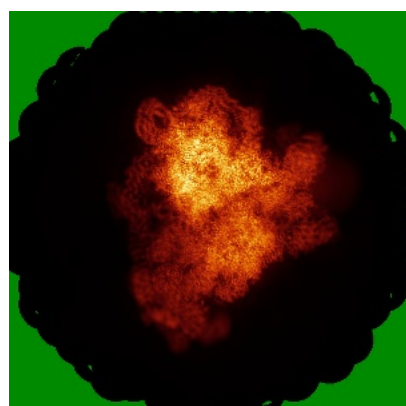


Z Index: 314

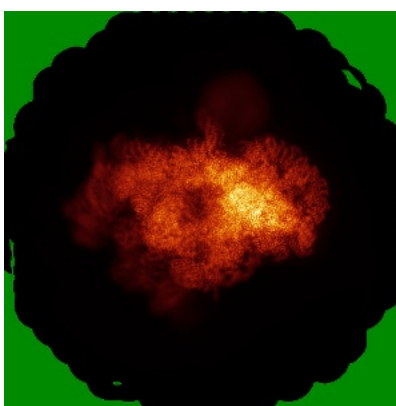
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

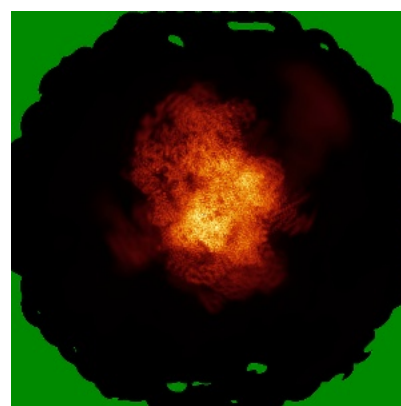
6.4.1 Primary map



X



Y

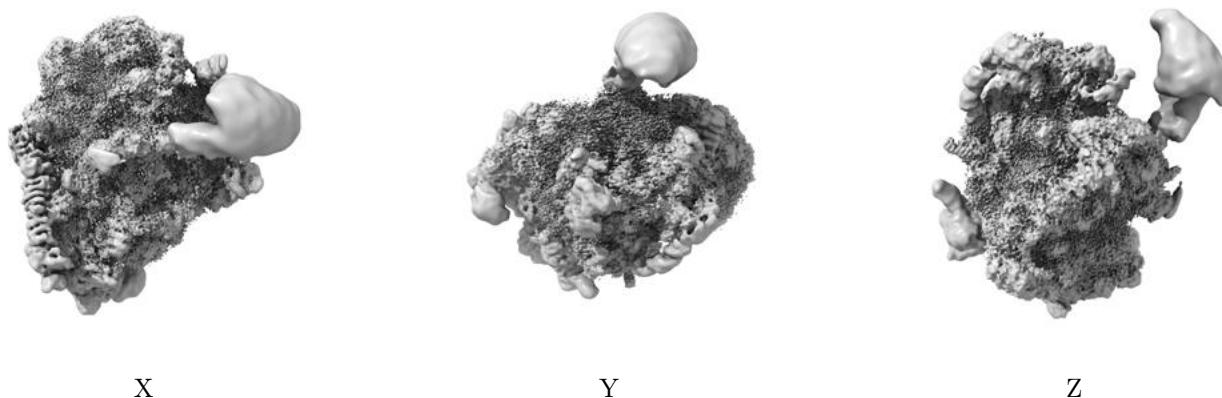


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

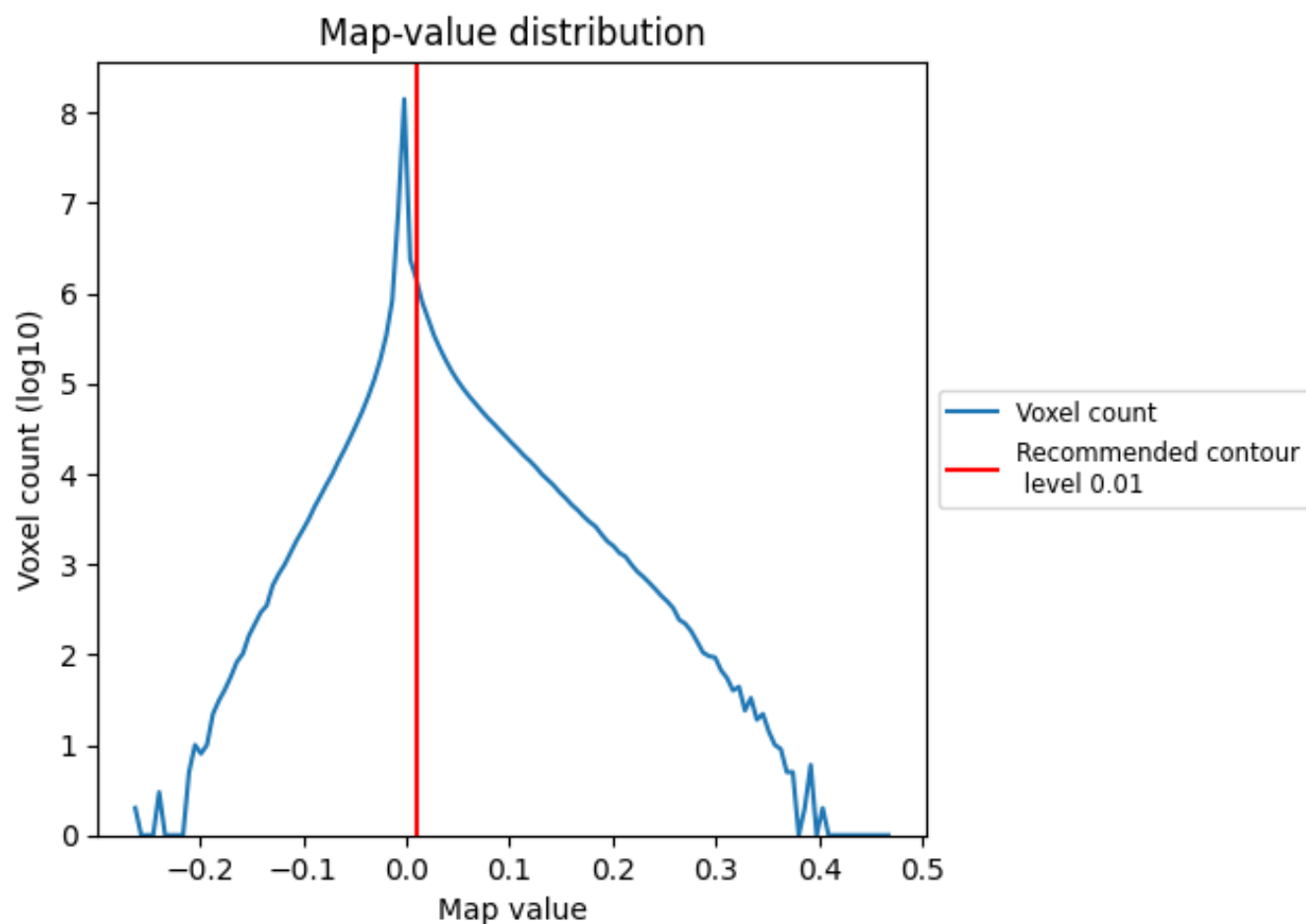
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

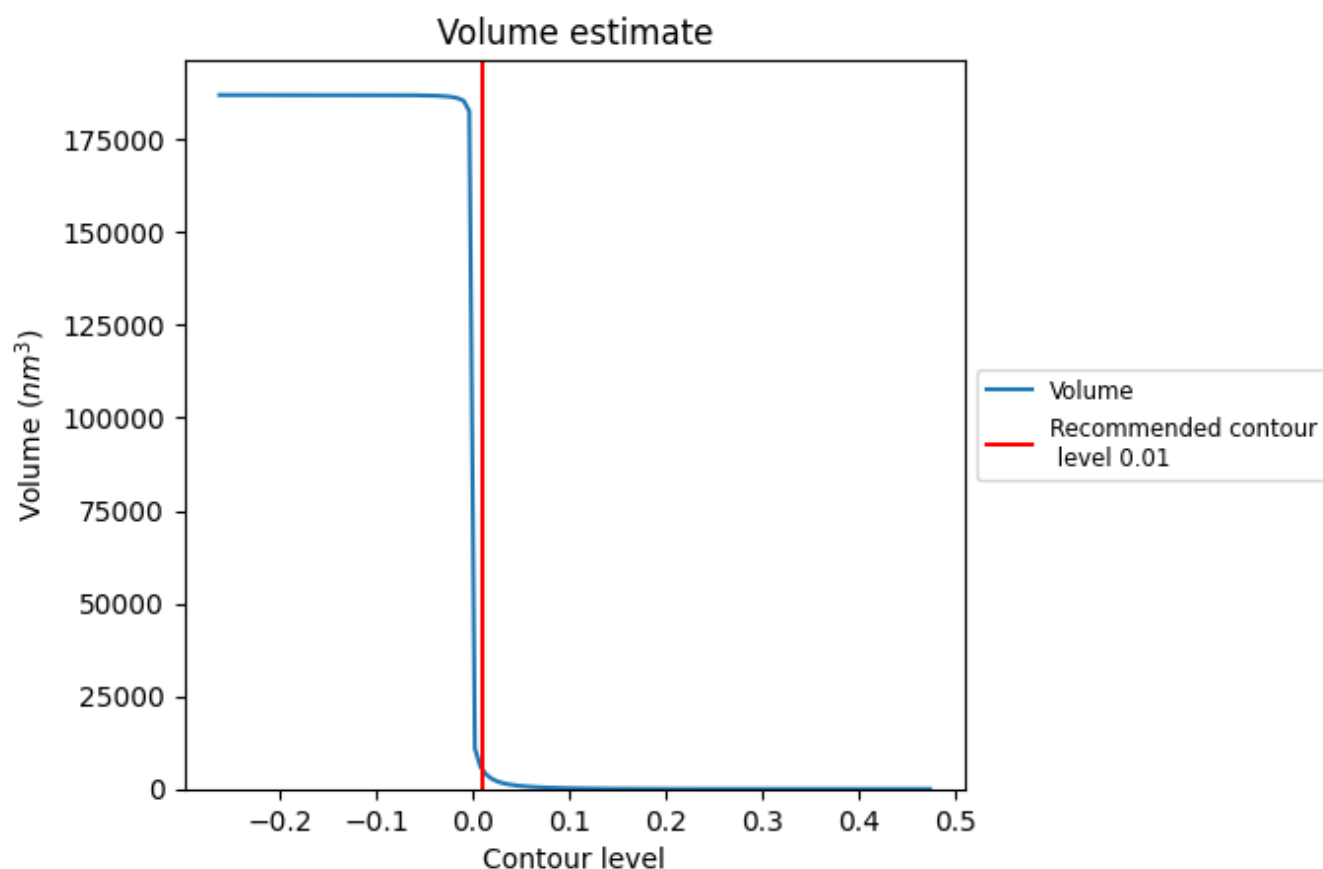
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

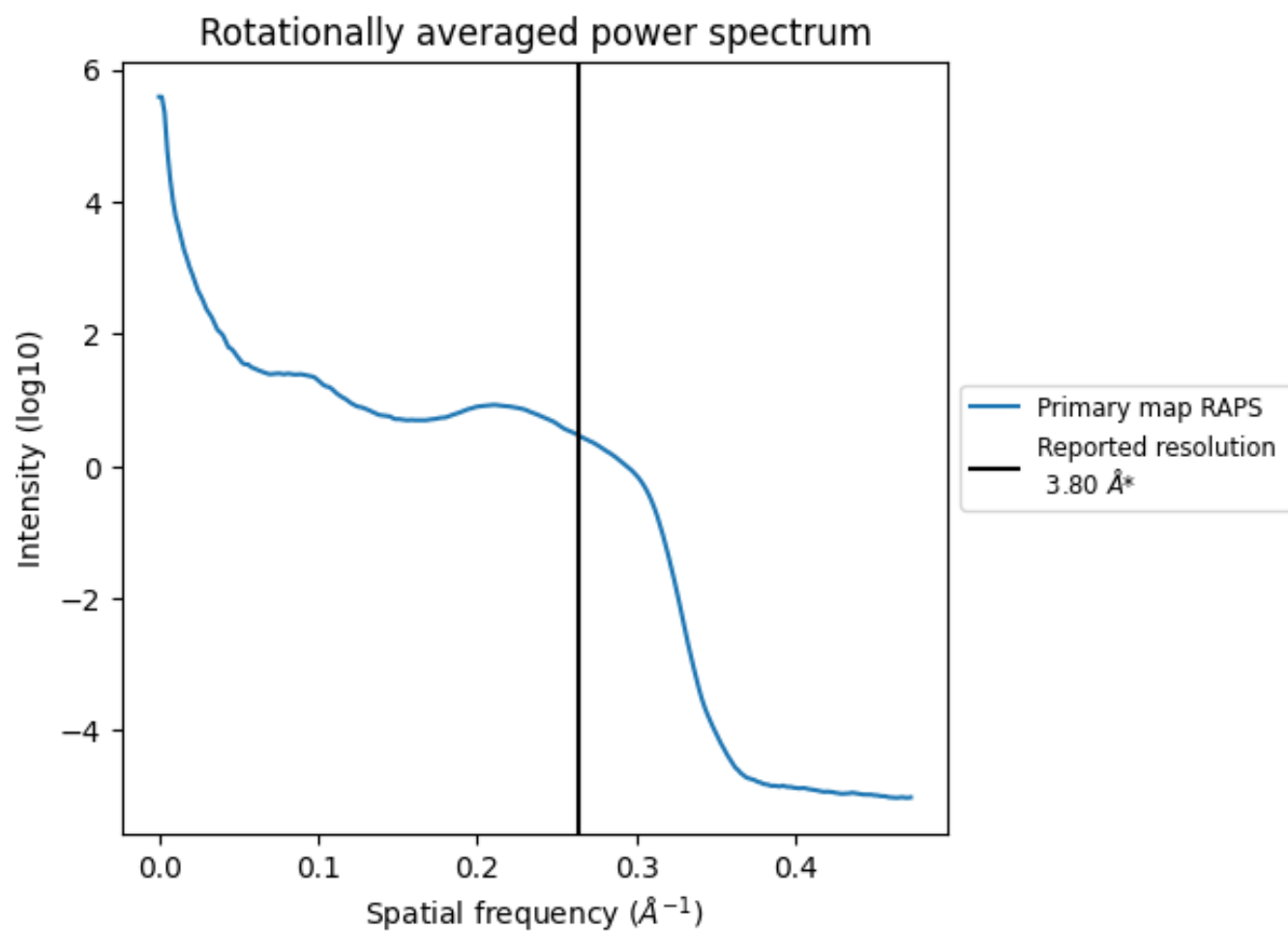
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5032 nm^3 ; this corresponds to an approximate mass of 4545 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

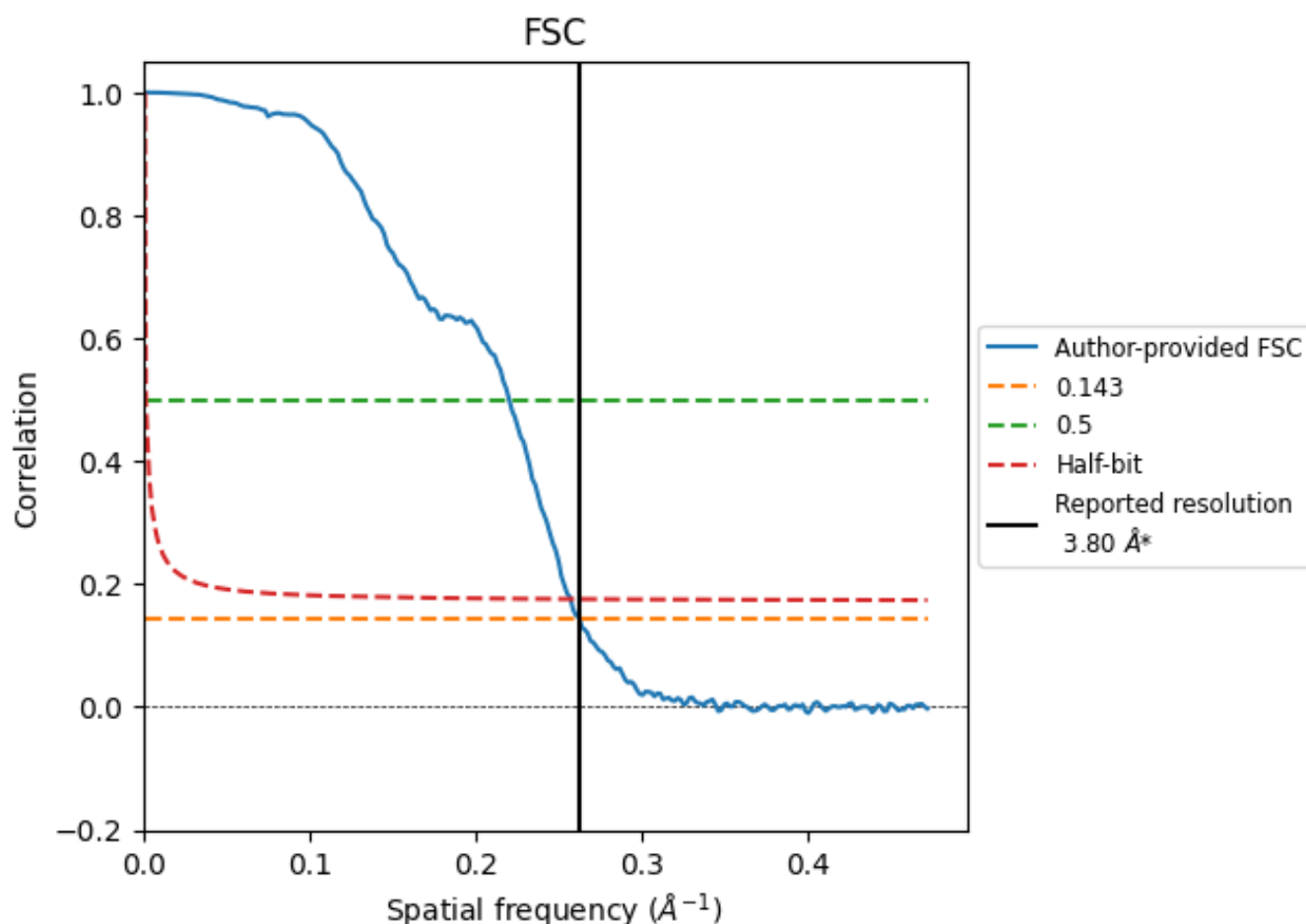


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.263 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.81	4.54	3.89
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

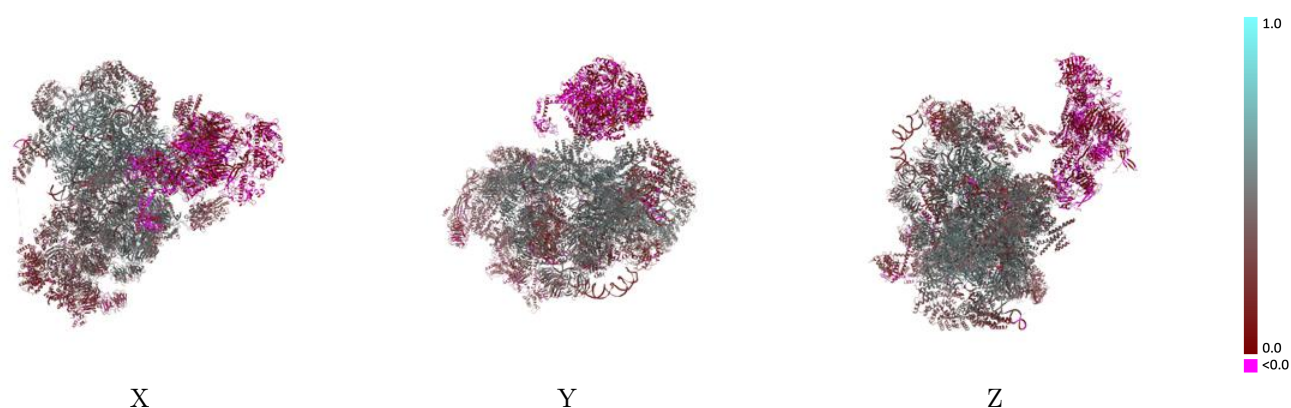
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-11808 and PDB model 7AJU. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)

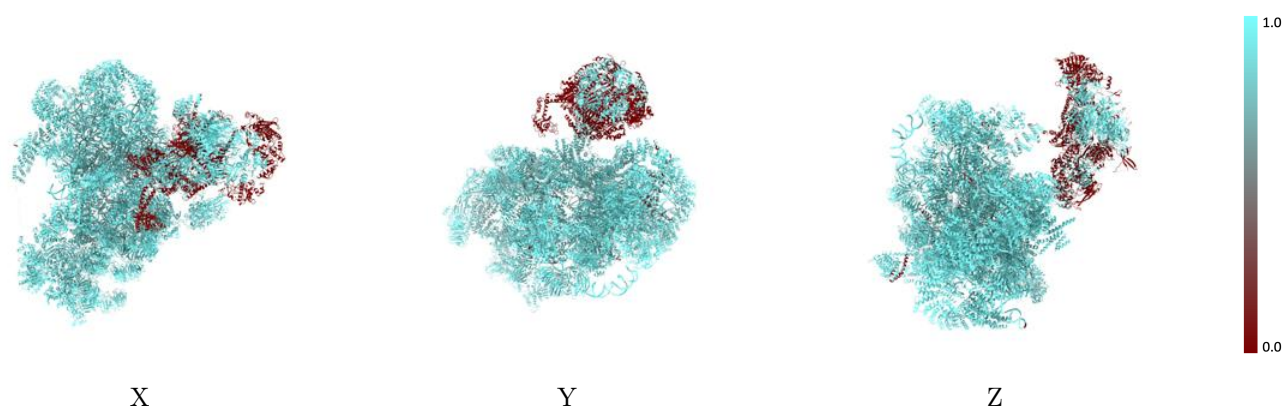
This section was not generated.

9.2 Q-score mapped to coordinate model [i](#)



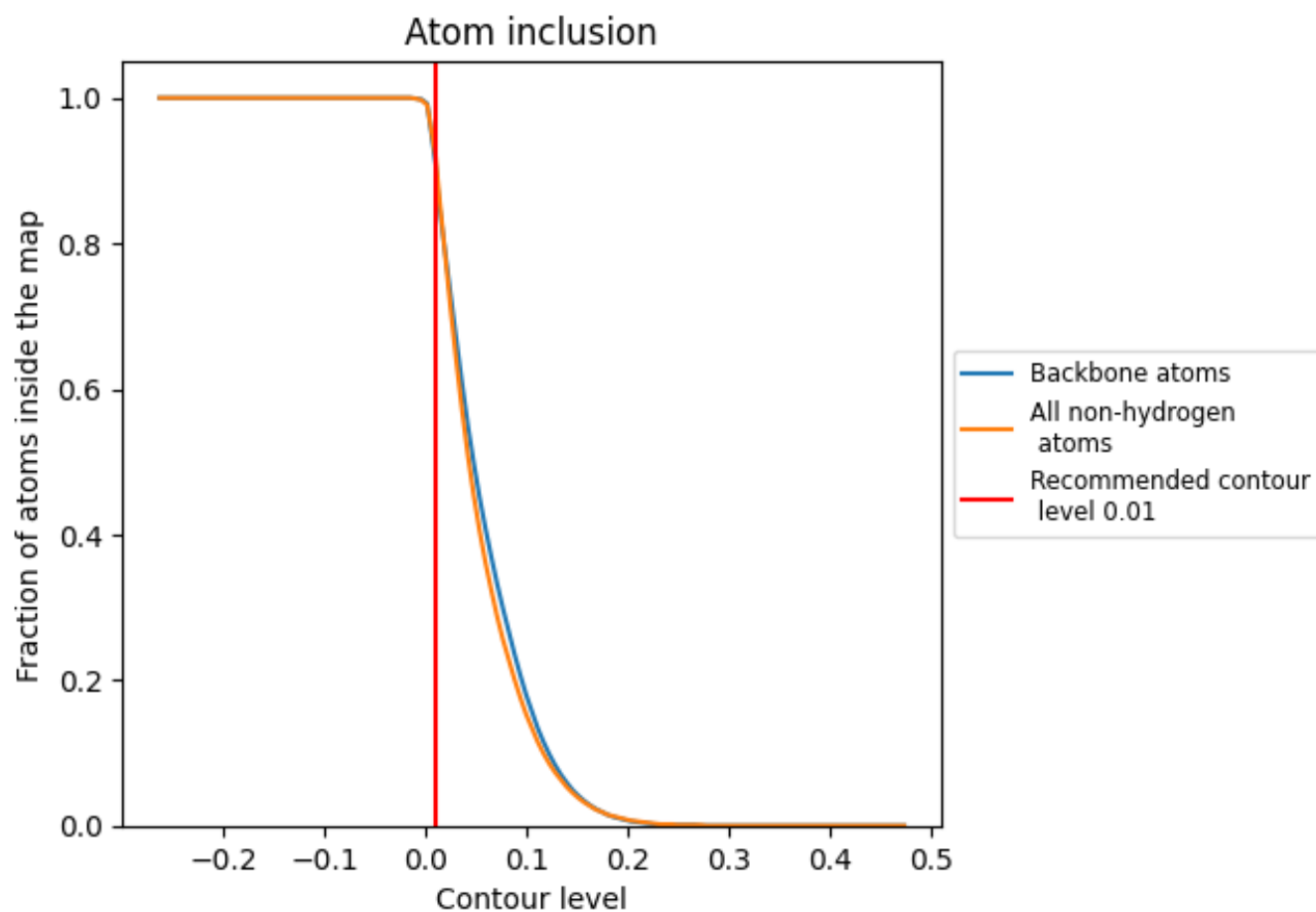
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9180	 0.3660
CA	 0.9820	 0.5320
CB	 0.9630	 0.3860
CD	 0.9740	 0.4510
CE	 0.9670	 0.3810
CF	 0.9510	 0.4100
CG	 0.9710	 0.5040
CH	 0.9900	 0.5070
CI	 0.9530	 0.4040
CJ	 0.9470	 0.4640
CK	 0.9780	 0.4530
CL	 0.9620	 0.4670
CM	 0.9870	 0.4770
CN	 0.9760	 0.3130
D2	 0.9290	 0.2450
D3	 0.9780	 0.4550
D4	 0.9470	 0.3430
DA	 0.9760	 0.5000
DE	 0.9900	 0.5770
DF	 0.9820	 0.4750
DG	 0.9930	 0.4920
DH	 0.9720	 0.4760
DI	 0.9870	 0.5300
DJ	 0.9830	 0.5540
DL	 0.9920	 0.5440
DN	 0.9760	 0.5150
DO	 0.9870	 0.5100
DQ	 0.9800	 0.4990
DS	 0.7790	 0.2510
DT	 0.7880	 0.3220
DW	 0.9780	 0.5690
DX	 0.9720	 0.5200
DY	 0.9820	 0.5460
Db	 0.9820	 0.5430
Dc	 0.9940	 0.4990



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
EA	 0.5550	 -0.0160
EB	 0.3590	 0.0030
EC	 0.5350	 0.0130
ED	 0.7980	 0.0450
EE	 0.8410	 0.0480
EF	 0.8530	 0.0380
EG	 0.8260	 0.0300
EH	 0.1750	 0.0420
EI	 0.5400	 0.0270
EJ	 0.1710	 0.0100
EK	 0.3440	 0.0230
EN	 0.2480	 0.0260
JD	 0.9160	 0.2530
JF	 0.9440	 0.1520
JG	 0.9410	 0.2340
JH	 0.9590	 0.1490
JI	 0.7860	 0.1720
JJ	 0.9760	 0.4860
JL	 0.9250	 0.3520
JM	 0.9550	 0.4290
JP	 0.9860	 0.5510
UA	 0.9790	 0.5040
UB	 0.9330	 0.1870
UC	 0.9690	 0.4960
UD	 0.9730	 0.3120
UE	 0.9530	 0.3570
UF	 0.9840	 0.4230
UG	 0.9810	 0.5010
UH	 0.9720	 0.1410
UI	 0.9690	 0.1760
UJ	 0.9340	 0.3300
UK	 0.9130	 0.3730
UL	 0.9840	 0.4080
UM	 0.9720	 0.4070
UN	 0.9770	 0.4800
UO	 0.9410	 0.2560
UP	 0.9330	 0.3080
UQ	 0.9640	 0.2520
UR	 0.9620	 0.4270
US	 0.9320	 0.1770
UT	 0.9780	 0.4140
UU	 0.9820	 0.4700

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
UV	 0.9740	 0.3420
UX	 0.9580	 0.5330